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produce 2 different mRNAs, one encoding a long form (bcl-XL), the other a short form (bcl-XS), lacking a stretch of 63 amino acids, by differential splicing of the 2nd coding exon to a more proximal 5'-splice donor within the 1st coding exon. Bcl-XS acts as a dominant negative regulator to bcl-XL activity, so it is preferable to use the bcl-XL cDNA for expression. The gene may be modified to facilitate interaction with costimulatory Bax protein and inhibit interaction with antagonistic Bad protein, by modification of the Bcl-2 homology domains BHI and/or BH2. The bcl-XL gene may be introduced into T-cells in vivo or ex vivo via gene transfer using a vector for HIV infection gene therapy, to augment intracellular bcl-XL protein levels and protect from cell death. A corresponding antisense oligonucleotide or expression vector may be used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                 therapy of e.g. autoimmune disease, graft rejection or graft-
versus-host disease, to induce cell death (e.g. apoptosis) and
down-regulate the immune response in a T-lymphocyte population.
Sequence 926 BP; 220 A; 249 C; 264 G; 193 T;
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ö aggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgc 397 geteageccageaacgetteacecaggtetecgaegaacttttteaagggggeeceaaet 277 ggggccgccttgtagccttcttttctctttggggctgcactgtgtgctgagagtgtcaaca 337 458 acggggccctggaggaggaggcgcgtctgcgggagggaactgggcatcagtgaggacag 517 724 ACAATGCAGCAGCCGAGAGCCGAAAGGGCCCAGGAACGCTTCAACCGCTGGTTCCTGACGG 783 98 ccgggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157 tegagaccegetteeggegeacettetetgatetggeggeteagetggeatgtgaceeeag 217 424 TTGAACTGCGGTACCGGCGGGCATTCAGTGACCTGACATCCCAGCTCCACATCACCCCAG 483 0; Gaps 484 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACT 544 GGGGTCGCATTGTGGCCCTTTTCTCCTTCGGCGGCCACTGTGCGTGGAAAGCGTAGACA Score 131; DB 1; Length 926; Pred. No. 8.7e-24; 0; Mismatches 190; Indels Query Match 22.5%; Best Local Similarity 56.3%; Matches 245; Conservative C 518 tgctgacggggccg 532 784 GCATGACTGTGGCCG 798 158 338 218 278

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25-JUN-1999 (first entry)
Base sequence of the plasmid pRx-Bcl-xl-bsr.
Base sequence of the plasmid px-Bcl-xl-bsr.
Crmh; bcl-z; bcl-xl; Fillp; survivin; IAP; ILP; adenovirus; cancer; crmh; bcl-z; bcl-xl; Fillp; survivin; IAP; ILP; adenovirus; cancer; autoimmune disease; graft rejection reaction; inflammation;
                                                                                                                                                                                                                                                       08-SEP-1997; JP-259235.
(RPRG-) RPR GENCELL ASIA PACIFIC INC.
                              X33182 standard; DNA; 7372 BP.
                                                                                                                                                   inflammatory disease; ss. Synthetic.
                                                                                                                                                                                                                                         07-SEP-1998; J04010
                                                                                                                                                                                     Hômo sapiens.
WO9913073-A2.
18-MAR-1999.
RESULT 15
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Whi; 99-243/28/20.

Whisperson through describes an apoptosis-resistant virus-sensitive cell Example 2; Page 41-45; 51pp; English.

Example 2; Page 41-45; 51pp; English.

The present invention describes an apoptosis-resistant virus-sensitive cell line into which an apoptosis resistance gene has been introduced.

The recombinant viruses generated are capable of expressing apoptosis-sociated genes. These can then be used in a variety of diseases for which the induction of apoptosis, is therapeutic. The recombinant viruses inhibition of harmful apoptosis, is therapeutic. The recombinant viruses are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an adenovirus vector capable of expressing an apoptosis-associated gene is introduced into animal cells, time required to induce cell death by apoptosis is shorter than that required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant gene introduced) is established and overcomes the problem. The present sequence represents the human Bcl-xl gene, and spoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the human Bcl-xl gene, and is used in an example from the present invention.

Sequence 7372 BP; 2353 A; 1749 C; 1649 G; 1621 T; WPI; 99-243728/20. 

ö 2541 2602 ACCTAGAGCCTTGGATCCAGGAGAACGCCGGCTGGGATACTTTTGTGGAACTCTATGGGA 2661 2662 ACAATGCAGCAGCCGAGAGCCGAAAGGGCCAGGAACGCTTCAACCGCTGGTTCCTGACGG 2721 2362 TTGAACTGCGGTACCGGCGGCGATTCAGTGACCTGACATCCCAGCTCCACATCACCCCAG 2421 517 togagaccogettecoggogeacettetetgatetggeggeteagetgeatgtgacceag 217 218 gctcagccagcaacgcttcacccaggtctccgacgaactttttcaagggggccccaact 277 98 ccgggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157 Gaps 398 ggctggtcgactggatccacagcagtgggggctgggcggagttcacagctctatacgggg 2422 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGGTAAACT 278 ggggccgccttgtagccttcttctcttttgggggctgcactgtgtgctgagagtgtcaaca 338 aggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgc 2542 AGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCACTTACCTGAATGACC 458 acggggccctggaggaggcgcgtctgcgggagggaactggggcatcagtgaggacag ; 0 Query Match 22.5%; Score 131; DB 1; Length 7372; Best Local Similarity 56.3%; Pred. No. 1.3e-23; Matches 245; Conservative 0; Mismatches 190; Indels 158 g 셤

Search completed: July 4, 2000, 01:26:24 Job time: 14671 sec

2722 GCATGACTGTGGCCG 2736 518 tgctgacgggggccg

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 which tissues they are most highly expressed in (see V59511 for described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human thymus BCL-XL DNA.*
BCL-XL, apoptos1s, cell death, cancer; neurodegenerative disease;
autoimmune disease; Parkinson disease; amylotrophic lateral sclerosis;
multiple sclerosis; ss.
                                                                                                                                                                                      aagctgaggcagaagggttatgtctgtggagctggcccggggaggggcccagcagctgac 120
                                                                                                                                                                                                                71 AAGCIGAGGCAGAAGGGIIAIGICIGIGGAGCIGGCCCCGGGGAGGCCCCAGCAGCIGAC 130
                                                                                                                                                                                                                                              ccgctgcaccaagccatgcgggcagctgagatgagttcgagacccgcttccggcgcacc 180
                                                                                                                                                                                                                                                                       131 CCGCTGCAACCAAGCCATGCGGGCAGCKGGAGATGAGTTCGAGACCCGGTTCCGGCGCCACC 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                             1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
                                                                                                                                                           11 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGTGGCAGACTTTGTAGGTTAT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Poly-nucleotide encoding new poly-peptide(s) that modify apoptosis - and related vectors, recombinant cells and antibodies, useful in assay and for control of cell death in e.g. claim 5; Page 94; 127pp; English.

This DNA may be expressed recombinantly for the production of a BCL-X protein, particularly with pcwV plasmids as vectors for expression in mammalian cell cultures. The protein has particular application in cancer cells (failure of programed cell death (PCD))
                                                                                                                                                                                                                                                                                                                                                                                                                 ttetetgatetggeggeteagetgeatgtgaceecaggeteageecageaacgetteaee
                                                                                                                                                                                                                                                                                                                   caggictccgacgaactititcaaggggccccaactggggccgccttgtagcctcttt
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0
                                                                        DB 1; Length 1864;
                               455 T;
                                                                                                   Indels
                             506 G;
                                                                     Score 423.6; DB 1;
Pred. No. 8.3e-96;
1; Mismatches 5;
                             403 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boise LH, Nunez G, Thompson CB; WPI; 95-052079/07.
                             494 A;
                                                                     72.7%;
98.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135. .836
/*tag= a
                                                                                    Best Local Similarity 98.6
Matches 426; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 agtgggggctgg 432
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05-JAN-1995.
22-JUN-1994; U07089.
22-JUN-1993; US-08144
                            1864 BP;
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Best Local
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                                                                                                                                                                         98 ccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157
                                                                                                                                                                                                                                                                                                                                                484 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGGTAAACT 543
                                                                                                                                                                                                           158 tcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccag 217
                                                                                                                                                                                                                                                                             424 TTGAACTGCGGTACCGGCGGCGTTCAGTGACCTGACATCCCAGCTCCACATCACCCCAG 483
                                                                                                                                                                                                                                                                                                                                                                                                                  544 GGGTCGCATTGTGGCCTTTTTCTCCTTCGGGGGCACTGTGCGTGGAAAGCGTAGACA 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                      aggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgc 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         664 ACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGATACTTTTGTGGAACTCTATGGGA 723
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                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inducting or preventing death of T cells by bcl-XL protein regulation used to increase survival of HIV infected cells or to down:regulate immune responses in immune diseases bisclosure; Page 51-52; 76pp; English.

This sequence encodes human bcl-XL protein, which protects T-lymphocytes against cell death. The genomic bcl-X gene may
                                                                                                                                                                                                                                                                                                                 geteageeceageaacgettcacceaggtetecgacgaactttttcaagggggeeceaact
                                                                                                                                                                                                                                                                                                                                                                                ggggccgccttgtagccttctttcttttggggctgcactgtgtgctgagagtgtcaaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, 501-XL, T-lymphocyte; cell death; gene therapy; HIV; AIDS; antisense; Immune disorder; autoimmune disease; graft rejection; graft-versus-host disease; apoptosis; adoptive immunotherapy; ss.
 or neurodegenerative and autoimmune diseases (premature PCD), e.e.
                                                                                                    Score 131; DB 1; Length 926;
Pred. No. 8.7e-24;
0; Mismatches 190; Indels
                                                    193 T;
                                                    264 G;
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                                                    249 C;
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                                                                                                      22.5%;
56.3%;
                                                    220 A;
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                                                                                                                                      Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                518 tgctgacgggggccg 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  784 GCATGACTGTGGCCG 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995; US-481739.
(ARCH-) ARCH DEV CORP.
(USNA ) US SEC OF NAVY.
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                                                                                                    Query Match
Best Local Similarity
                                                  926 BP;
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                                   sclerosis.
                                                    Sequence
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Human secreted protein; gene 120 clone HGBG264.

Human secreted protein; fusion protein; gene therapy; protein therapy;

Human; secreted protein; fusion protein; gene therapy; protein therapy;

Human; secreted protein; fusion protein; gene therapy; protein therapy;

diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukeemia;

developmental abnormality; foetal deficiency; blood; allergy; renal; dinflammation; ischaemic shock; Alzheimer's disease; restenosis; AnDS;

cognitive disorder; schlzophrenia; prostate; obesity; osteoclast; thymus;

osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;

endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                       V59630 standard; DNA; 1864 BP
                                                                                              19-JAN-1999 (first entry)
                                                                                                                                                                                                                                                           US-038621.
US-040161.
US-040163.
US-040333.
US-040334.
US-040334.
US-043311.
US-043313.
US-043569.
US-043576.
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US-043578.
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US-043674.
US-047492.
US-047500.
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US-043670.
US-043671.
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US-047581.
US-047582.
US-047583.
US-047584.
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US-047612.
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421 agtgggggctgg 432
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                     421 AGTGGGGGCTGG 432
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06-MAR-1998; U04493.
02-OCT-1997; US-06106
07-MAR-1997; US-03865
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23-MAY-1997;
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11-APR-1997;
23-MAY-1997;
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07-MAR-1997;
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23-MAY-1997;
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23-MAY-1997;
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11-APR-1997;
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                                                     RESULT 12
V59630
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New isolated human genes and the secreted polypeptide(s) they encode new insolated human genes and treatment of e.g. cencers, neurological useful for diagnosis and treatment of e.g. cencers, neurological disorders, immune diseases, inflammation or blood disorders a classification or blood disorders disorders a nucleic acid molecule designated Gene 120 from This sequence represents a nucleic acid molecule designated Gene 120 from the human cDNA clone HGBG264 (deposited as clone ATCC 97902 and ATCC 20904B) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin compared to the human protein only.

The invention relates to 186 novel genes and their fragments (nucleic acid sequences: V95811-V59812; anino acid sequences W74711-W75026) which are useful for preventing, treating or ameliorating medical conditions can be compared by determining the amount of the new polypeptides in a sample combinance of mutations in the new polynuclectides. Specific uses are described for each of the 186 polynuclectides, based on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA) HUMAN GENOME SCI INC.

(HUMA) HUMAN GENOME SCI INC.

Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA, Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS, Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;

P-SDB; W74048.
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22-AUG-1997; US-0569110.
22-AUG-1997; US-056911.
05-SEP-1997; US-057650.
05-SEP-1997; US-057761.
12-SEP-1997; US-057761.
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US-056889.
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US-047632.
US-047633.
US-048964.
US-048974.
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US-056894.
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22-AUG-1997;
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22-AUG-1997;
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16-JUL-1997;
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22-AUG-1997;
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22-AUG-1997;
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22-AUG-1997;
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An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w

Disclosure; Page 38; 52pp; English.

The present sequence is described as a derivative of the mouse close x25133 and encodes Bcl-w protein (see Y05533), a core-wivival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates cand which is essential for spermatogenesis. The invention relates candentification of molecules and genetic sequences useful for the inducting or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing ertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene car mutation is at least one allele of the human or murine bcl-w gene core in a gene associated with bcl-w. Such animals have disorganised conter major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including entities and are substantially infertile, but possess no cher major abnormalities and inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce
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      16-SEP-1998; AU0764.
16-SEP-1997; AU-009228.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Adams J. Cory S, Gibson L, Koentgen F, Print C;
P-PSDB; Y05533.
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Claim 2; Fig 12A-12D; 12Opp; English.

This is the nucleotide sequence of the cDNA clone Bcl-like (HAICH29), used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, various allergies, and as anti-infectious agents. The products can also be used for detection and diagnosis. Sequence 1098 BP; 264 A; 279 C; 325 G; 230 T;
                                                                      20-NOV-1998 (first entry)
Nucleotide sequence of the cDNA clone Bcl-like (HAICH29).
Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction; immunological disorder; autoimmune disease; anti-infectious agent; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies
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                                                                                                                                                                                                                              /product= "Bcl-like (HAICH29) protein"
                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
Feng P, Gentz RL, Krissansen GW, Ni J, Rosen CA,
Su JY;
                                                                                                                                                                      Location/Qualifiers 1.1098
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                                      V41925 standard; cDNA; 1098 BP.
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21-JAN-1997; US-034204.
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WO9913710-A1
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                                          Gaps
                                                         1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
                                                                     1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
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Nucletc acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
                                                                                                                                                                                                                                                                                                         cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg
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                         Length 581;
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117
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Pred. No. 4.2e-120;
0; Mismatches 37;
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Adams JM, Cory S, Gibson LM, Holmgreen SP;
WPI; 97-489635/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis; degenerative disease; ss
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/product= bcl-w
                          89.5%;
93.6%;
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 106
                                          Matches 544; Conservative
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27-MAR-1996; AU-008965.
                                   Local Similarity
 BP;
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02-OCT-1997.
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Claim 3; Page 50-51; 86pp; English.
This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene this sequence encodes a novel gene, bcl-w, from the moulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   caggictccgacgaactititcaaggggccccaactggggccgccttgtagccttctit 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 CAAGICCAGGAITGGAICGIGGCCIACCIGGAGACACGICIGGCIGACIGGAICCACAGC 420
                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse bcl-w gene derivative.
Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacggggggccgtggcactg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 581;
                                                                                                                                                                                                                                                                 117 T;
                                                                                                                                                                                                                                                                                                                     Query Match

85.9%; Score 501; DB 1; Length 58

Best Local Similarity 91.4%; Pred. No. 5.5e-115;

Matches 531; Conservative 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                 195 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 ggggccctggtaactgtaggggccttttttgctagcaagtg
                                                                                                                                                                                                                                                                 164 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X25135 standard; DNA; 581 BP
                                                                                                                                                                                                                                                                   105 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X25135;
05-JUL-1999 (first entry)
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                                                                                                                                                                                                                                                                 581 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      animal model; ss.
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aagctgaggcagaagggttatgtctgtggagctggcccggggagggcccagcagcagct 120 61 AAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCGACC 180

61

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181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240

ttototgatotggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc

181

241 caggtctccgacgaacttttcaaggggccccaactggggccgccttgtagccttcttt

GTCTTTGGGGCTGCCCTGTGTGTGTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360 361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420

361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGGACTGGATCCACAGC 

421

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541

301 ctctttgggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga

480

540

481 CGTCTGCGGGGGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG

ggggccctggtaactgtaggggccttttttgctagcaag 579

Mouse bcl-w gene. Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;

animal model; ss.

W09913710-A1 25-MAR-1999

16-SEP-1997; AU-009228. 16-SEP-1998; AU0764.

X25133 standard; DNA; 581 BP. 05-JUL-1999 (first entry)

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RESULT

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for modulating programmed cell death

Disclosure: Columns 13-16; 26pp; English.

The present sequence encodes rat bcl-y protein (Rbcl-y). The present sequence encodes rat bcl-y protein (Rbcl-y). Rbcl-y and pecification also describes human bcl-y protein (Rbcl-y). Rbcl-y and pecification also describes human bcl-y protein (Hbcl-y). Rbcl-y and Bbcl-y are homologues of the bcl-2 protein thought to be involved in programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y and pbcl-y proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used to treat subjects suffering from: strokes, head trauma, the cell death pathway. If they act as cell death inhibitors, they may be used to treat subjects suffering from: strokes, head trauma, alzehmer's Disease, neural and muscular degenerative diseases.

Caspecially multiple sclerosis), mycocadial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral cell death, aging, spinal cord injuries and amyotrophic lateral cell death, aging, spinal cord injuries and amyotrophic lateral cell neath as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites.

Sequence 579 BP: 111 A; 157 C; 198 G; 113 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA encoding the rat bc1-y protein.

Rat bc1-y protein; Rbc1-y; human bc1-y protein; Hbc1-y; bc1-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                     540
                                                                                                                                                                                                                             481 CGTCTGCGGGAGGGGAACTGGCCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540
                             CAAGTGCAGGATTGGATGGTGACCTACCTGGACACGCTTGGCTGACTGGATCCACAGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel bcl-y homologues of the rat and human bcl-2 protein - useful
                                                                                                      agtgggggctggggggttcacagctctatacggggacggggccctggaggaggcgcgg
                                                                                                                                                                                  cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacggggggccgtggcactg
                                                                                                                                                                                                                                                                                                                    ggggccctggtaactgtaggggccttttttgctagcaag 579
X15945 standard; cDNA; 579 BP.
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25-NOV-1997; 978523.
23-FEB-1996; US-012201.
11-FEB-1997; US-798897.
25-NOV-1997; US-978523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99-214150/18.
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US5883229-A.
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An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w

Scalaim 3: Page 3: 52pp: English.

The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see Y0531), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic invention relates provided for the treatment of infertility, or canimals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or more increased in a gene or in a gene associated with bol-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined the infertile, but possess no other major abnormalities as determined therapeutic molecules including genetic sequences capable of inducting, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.
                                                                                                                                                                                                                                                         Gibson L, Koentgen F, Print C;
                                                                                                                                                                                                                                 (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Adams J. Cory S, Gibson L, Koentgen F, Print
WPI; 99-243890/20.
                                                                                                                                                                                                                                                                                                       P-PSDB; Y0553.
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0; Gaps

1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60 

q ð

89.7%; Score 523; DB 1; Length 579; 94.0%; Pred. No. 2.1e-120; 1ve 0; Mismatches 35; Indels

Query Match
Best Local Similarity 94.0
Matches 544; Conservative

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Proceedings of the process of the pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caggiciccgacgaactititcaagggggccccaactggggccgccttgtagcctictti 300
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                                                                                                                                                                                                                                                              Novel bcl-y homologues of the rat and human bcl-2 protein
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0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             572; Conservative
                                                                                     23-FEB-1996; US-012201.
11-FEB-1997; US-798897.
25-NOV-1997; US-978523.
                                                                                                                                                                   (COCE-) COCENSYS INC.
                                                                 25-NOV-1997; 978523
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                                                                                                                                                                                                                 WPI; 99-214150/18.
P-PSDB; W97392.
                                                                                                                 11-FEB-1997;
25-NOV-1997;
                 US5883229-A.
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Matches 57
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The mammalian bcl.y genes froode a protein that is a member of the bcl-2 family components in the cell death pathway. The bcl-2 family have both apoptoric activity and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired.

Sequence 579 BP; 111 A; 157 C; 198 G; 113 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360
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481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AAGCTGAGACAGAAGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGGA
                                                                                                                                                                               02-0CT-1998 (first entry)
Rat bcl-y gene.
ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 89.7%; Score 523; DB 1; Length 579; al Similarity 94.0%; Pred. No. 2.1e-120; 544; Conservative 0; Mismatches 35; Indels
                               541 ggggccctggtaactgtaggggccttttttgctagcaag 579
                                               /note= "No stop codon given'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  growth e.g. cancers
Claim 2; Column 13/14; 27pp; English.
                                                                                                                                                                                                                                                     Location/Qualifiers
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/product= bcl-y
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23-FEB-1996; US-012201.
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(COCE-) COCENSYS INC.
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ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
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otherwise facilitating spermatogenesis
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                                             Length 581;
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                                           Score 573; DB 1;
Pred. No. 1e-132;
0; Mismatches 5;
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       or which can induce infertility. 581 BP; 104 A; 155 C;
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99.1%;
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23-FEB-1996; US-012201.
11-FEB-1997; US-798897.
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WPI; 98-446079/38.
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CDNA encoding the human bcl-y protein.

EDNA encoding the human bcl-y protein.

Ent bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;

programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;

head trauma; Alzheimer's Disease; neural; muscular degenerative disease;

multiple sclerosis; myocardial infarction; vitally induced cell death;

aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;

premature cell death; cell death stimulator; prolonged cell life span;

Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
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producing recombinant protein for use in treating uncontrolled cell
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181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl.w gene or in a gene associated with bcl.w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein associated will but a solution of the human bisclosure; Page 38; 52pp; English.

The present sequence is described as a derivative of the human bcl-w gene (see X25132) and encodes Bcl-w protein (see Y05532), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for sperimatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and generic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing provided for the treatment of infertility, or for reducing fertility and inducing or the treatment of infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w
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Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
                                                                           241 CAGGICTCCGACGAACITITICAAGGGGCCCCCAACIGGGGCCGCCTIGIAGCCTICITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce
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16-SEP-1997; AU-009228.
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WO9913710-A1.
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Ouery Match 100.0%; Score 583; DB 1; L
Best Local Similarity 100.0%; Pred. No. 3.5e-135;
Matches 583; Conservative 0; Mismatches 0;
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Problem 10031 (10033).

An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w

Sclaim 3; Page 31; 52pp; English.

Claim 3; Page 31; 52pp; English.

The present sequence is the human bcl-w gene encoding Bcl-w protein (see Y0530), a pro-survival member of the Bcl-2 family which is undely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male sequences useful for inducing or reducing fertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals the at least one allele of the human or infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of 480 481 ogtctgogggagggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540 540 301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360 421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGAGCGCGGG 480 181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240 121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180 121 ccecrecaccarecarecaecaecrecaecresaerresaerresaeaccescrrccaececaec 180 181 ITCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240 241 caggictccgacgaactititcaagggggccccaaciggggccgcctigtagccitctit 300 1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60 Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility; 421 agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg 481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 541 ggggccctggtaactgtaggggccttttttgctagcaagtgaa 583 25-MAR-1999.
16-SEP-1998, AU0764.
16-SEP-1997, AU-009228.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Adams J. COTY S, Glbson L, Koentgen F, Print C;
P-PSDB; Y05530. X25132 standard; DNA; 581 BP 05-JUL-1999 (first entry) Human bcl-w gene. animal model; ss. Homo sapiens. WO9913710-A1. g g à g 셤 g 셤 δλ g g ð g ò ŏ ö ŏ ă

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July 3, 2000, 21:21:53; Search time 115.05 Seconds (without alignments) 1267.814 Million cell updates/sec
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CDNA encoding the
Rat bc1-y gene. Nu
CDNA encoding the
Mouse bc1-w gene.
Mouse bc1-w gene.
Mouse bc1-w gene d
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Sequence of bcl-2
Base sequence of t
Human BCL2 cDNA.
Mouse BCL-x gamma
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bcl-2 proft-oncoge
Sequence of bcl-2
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Human thymus BCL-X
Bax omega protein
CLNK en tymphoid B
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CMN encoding a hu
cSNT clone CB239. N
Human Cdn-3 DNA. N
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Human adenosine Al

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| Type III procollag Vector pAC3Al cont HSV-2 strain SB5 C HSV-2 strain SB5 C Genomic clone G11F Human thyroid tran HWAV-2 strain SB5 C HWAV-2 strain SB5 C HWAM D.D. receptor Immunoglobulin D-r Bak-2 gene. Screen Human Cdn-2 DNA. N | ALIGNMENTS  1, 1  177 178 179 179 179 179 179 179 179 179 179 179  | tch 100.0%; Score 583; DB 1; Length 583; all Similarity 100.0%; Pred. No. 3.5e-135; all Similarity 111111111111111111111111111111111111 |
|---|--|--|
| Q30849<br>T16508<br>V62162<br>V62176<br>Q55750<br>T05810<br>T05810<br>T14509<br>Q11709<br>Q11709  | ALIGNMEN.  trry)  2; cell survival; e disease; ss.  on/Qualifiers  2  ct a bcl-w  spry LTD.  on LM, Holmgreen spoptosis related al, e.g. for treat apoptosis related al, e.g. for treat if English. a novel human gene an adult brain li an ovel human gene an adult brain li degenerative dise farct, muscular de virus infection op new lines, to i   | Score  Pred.  Pred.  Misman  Sagacacac  Sagacacac  Sagacacac  Cctgtggag                RCTGTGGAG              RGCTGGAG  Sagctgag  Sagctgag  Sagctgag  Sagctgag  Sagctgag   |
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| $\begin{array}{cccccccccccccccccccccccccccccccccccc$  | standard; DNA; 1998 (first e apoptosis; bcl is; degeneratipiens. Locat is; degeneratipiens. Locat 1997, Audulgo. 1997, Audulgo. 1996, Au-00896, Au | similarity<br>35. Conser<br>35. Conser<br>10. Conser<br>11. 11. 11. 11. 11. 11. 11. 11. 11. 11.  |
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cc dominant negative regulator to bcl-XL activity, so it is preferable to use the bcl-XL cDNA for expression. The gene may be modified to facilitate interaction with costimulatory Bax protein and inhibit interaction with antagonistic Bad protein, by modification of the Bcl-2 homology domains BH1 and/or BH2. The bcl-XL gene may be introduced into T-cells in vivo or ex vivo via gene transfer using a vector for HIV infection gene therapy, to augment intracellular cbcl-XL protein levels and protect from cell death. A corresponding antisense oligonucleotide or expression vector may be used in gene chrange of antisense oligonucleotide or expression vector may be used in gene continuate disease, to induce cell death (e.g. apoptosis) and coverus-host disease, to induce cell death (e.g. apoptosis) and coverus-host disease, to induce cell death (e.g. apoptosis) and sequence 926 BP; 220 A; 249 C; 264 G; 193 T;
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                                      Gaps
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DB 1; Length 926;
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23.2%; Score 134.6; DB 1
58.3%; Pred. No. 2.6e-27;
                                        Matches 236; Conservative
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Best Local Similarity
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RESULT 15
X33182
ID X33182 standard; DNA; 7372 BP.
AC X33182
DE X33182
DE Base sequence of the plasmid pRx-Bcl-xl-bsr.
DE Base sequence of the plasmid pRx-Bcl-xl-bsr.
WW Cowpox virus; bsr; viral vector; expression; apoptosis; resistance;
KW autoimmune disease; graft rejection reaction; inflammation;
KW inflammatory disease; ss.
OS Synthetic.
OS Homo sapiens.
PN WO9913073-A2.
PD 18-WAR-1999.
PR 07-SEP-1997; JP-259235.
PR (RPRG-) RPR GENCELL ASIA PACIFIC INC.
PR (RPRG-) RPR GENCELL ASIA PACIFIC INC.
PI Hamada H;
PR AND 99-243728-20.
PR New apoptosis-resistant virus-sensitive cell
PR New apolionis-sensitive cell
PR Sxample 2; Page 41-45; 51pp; English.
CC The present invention describes an apoptosis-resistant virus-sensitive ccl The present invention describes are capable of expressing apoptosis-
CC The recombinant viruses generated are capable of expressing apoptosis-
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2692 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG 2736

Search completed: July 4, 2000, 01:26:28

Job time: 14675 sec

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which the induction of apoptosis by gene transfer, or where the inhibition of harmful apoptosis, is therapeutic. The recombinant viruses are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory deliamatory diseases. Prior arts have concountered the problem where if an adenovirus vector capable of expressing an apoptosis-associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of time required to reduce cell death by apoptosis is shorter than that required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated contains apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the base sequence of the problem. The present sequence represents the human Bcl-xl gene, and is used in an example from the present invention.

Sequence 7372 Bp; 2353 A; 1749 C; 1649 G; 1621 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2392 ACCIGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 2451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2332 AGCAAGCGCTGAGGGAGGCAAGGCGACTTTGAACTGCGGTACCGGCGGCGCATTCAGTG 2391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2632 GCTGGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCC 2691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2572 CAGCTIGGAIGGCCACTIACCIGAAIGACCACCIAGAGCCIIGGAICCAGGAGAACGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.2%; Score 134.6; DB 1; Length 7372; 58.3%; Pred. No. 4.5e-27; tive 0; Mismatches 169; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        488 gggagggaactgggcatgagtgagcacagtggtgacggggccg 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 236; Conservative
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Best Local Similarity
                       88888888888888888888888
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which tissues they are most highly expressed in (see V59511 for described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human thymus BCL-XL DNA. "I BCL-XL; apoptosis; cell death; cancer; neurodegenerative disease; autoimmune disease; Parkinson disease; amylotrophic lateral sclerosis; multiple sclerosis; ss.
                                                                                                                                                                                250
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                                                                                                                                                                                                                                                                                                                                                                                                                         ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
                                                                                                                                                                                                                                                                131 CCGCTGCAACCAAGCCATGCGGGCAGCKGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 190
                                                                                                                                                                                                                                                                                                                                                                  360
                                                                                                                          atgcogaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60
                                                                                                   Gaps
                                                                                                                                                       11 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Poly-nucleotide encoding new poly-peptide(s) that modify apoptosis - and related vectors, recombinant cells and antibodies, useful in assay and for control of cell death in e.g. claim 5; Page 94; 127pp; English. This DNA may be expressed recombinantly for the production of a BCL-X protein, particularly with pcw V plasmids as vectors for expression in mammalian cell cultures. The protein has particular application in cancer cells (failure of programed cell death (PCD))
                                                                                                                                                                                                                                                                                             ttetetgacetggcegeteagetacacgtgaceccaggeteageccageaacgetteace
                                                                                                                                                                                                                                                                                                               TTCTCTGATCTGGCGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACACGCTTCACC
                                                                                                                                                                                                                                                                                                                                                      caggiticogacgaactiticcaagggggccctaactgggggccgictigiggcaticiti
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                                                                      DB 1; Length 1864;
                              455 T;
                                                                                                 Indels
                             506 G;
                                                                                              42;
                                                                    Score 364.4; DB 1
Pred. No. 7.6e-89;
1; Mismatches 42
                             403 C;
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                             494 A;
                                                                   62.7%;
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/*tag= a
                                                                   Query Match 62.73
Best Local Similarity 90.03
Matches 389; Conservative
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05-JAN-1995.
22-JUN-1994; U07089.
22-JUN-1993; US-081448.
(ARCH-) ARCH DEV CORP.
(UNMI ) UNIV MICHIGAN.
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                           1864 BP;
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                           Sequence
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128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
                                                                                                                                                                                                                      394 AGCAAGCGCTGAGGGAGGCAGGCGACGATTTGAACTGCGGTACCGGCGGGCATTCAGTG 453
                                                                                                                                                                                                                                                            acctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccaggttt 247
                                                                                                                                                                                                                                                                                               454 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513
                                                                                                                                                                                                                                                                                                                                 248 ccgacgaacttttccaaggggccctaactggggccgtctttgtggsattctttgtctttg 307
                                                                                                                                                                                                                                                                                                                                                                    514 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCG 573
                                                                                                                                                                                                                                                                                                                                                                                                            gggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtcc 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          428 gctgggcggacttcacagctctatacggggacggggccctggaggacgcacggcgtctgc 487
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used to increase survival of HIV infected cells or to down:regulate immune responses in immune diseases busines responses in immune diseases bisclosure; Page 51-52; 76pp; English.

This sequence encodes human bcl.*XL protein, which protects T-lymphocytes against cell death. The genomic bcl.*X gene may produce 2 different mRNAs, one encoding a long form (bcl.*XL), the other a short form (bcl.*XS), lacking a stretch of 63 amino acids, by differential splicing of the 2nd coding exon to a more proximal 5'-splice donor within the 1st coding exon. Bcl.*XS acts as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 aggattggatcgtggcctacctggagacacgtctggctgactggatccacagcagtggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; bcl.*XL; T-lymphocyte; cell death; gene therapy; HIV; AIDS; antisense; immune disorder; autoimmune disease; graft rejection; graft-versus-host disease; apoptosis; adoptive immunotherapy; ss.
or neurodegenerative and autoimmune diseases (premature PCD), e.c
Parkinson's disease, amylotrophic lateral sclerosis and multiple
                                                                                                                                                   ö
                                                                                                                 Length 926;
                                                         193 T;
                                                                                                           23.2%; Score 134.6; DB 1; Length 58.3%; Pred. No. 2.6e-27; ive 0; Mismatches 169; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   754 AGGAACGCTTCAACCGCTGGTTCCTGACGGCCATGACTGTGGCCG 798
                                                         264 G;
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/product= Human bcl-XL protein
                                                       249 C;
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                                                     220 A;
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                                                                                                                              Best_Local Similarity 58.3
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAY-1995; US-435518.
07-JUN-1995; US-481739.
(ARCH-) ARCH DEV CORP.
(USNA.) US SEC OF NAVY.
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                                                       926 BP;
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WPI; 96-506159/50
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                                      sclerosis.
                                                         Sequence
                                                                                                               Query Match
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Human secreted protein; gene 120 clone HGBG264.

Human secreted protein; gene protein; gene therapy; protein therapy;

Human; secreted protein; fusion protein; gene therapy; protein therapy;

Human; secreted protein; fusion protein; gene therapy; protein therapy;

diagnosis; itssue; cancer; tumour; neurodegenerative disorder; leukaemia;

developmental abnormality; foetal deficiency; blood; allergy; renal; diffammune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;

inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;

cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;

osteoporosis; arthritis; testis; lung; thyroidtis; thyroid; disestion;
endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                      V59630 standard; DNA; 1864 BP
                                                                                                              19-JAN-1999 (first entry)
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US-043568
US-043578
US-043670
US-043670
US-043671
US-043671
US-043671
US-047501
US-047501
US-047581
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US-047582
US-047592
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US-047592
US-047593
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US-040336.
US-040626.
US-043311.
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421 agtggcggctgg 432
                      421 AGTGGGGGCTGG 432
                                                                                                                                                                                                                                                                                 06-MAR-1998; U04493.
02-OCT-1997; US-0610
                                                                                                                                                                                                                                                                                                                                  07-MAR-1997; U
07-MAR-1997; U
07-MAR-1997; U
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11-SEP-1998.
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                                                               RESULT 12
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This sequence represents a nucleic acid molecule designated Gene 120 from this sequence represents a nucleic acid molecule designated Gene 120 from the human cDNA clone HGBGZ64 (deposited as clone ATCC 97902 and ATCC 209048) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin protein as compared to the human protein only.

The invention relates to the human protein only.

The invention relates to 186 movel genes and their fragments (nucleic acid sequences: V59511-V59812; amino acid sequences W74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human genes and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders Claim 1; Page 353-354; 721pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA, Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS, Kyaw H, Laffeur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z; P-PSDB; W74848.
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05-SEP-1997; US-057650.
05-SEP-1997; US-057669.
05-SEP-1997; US-057761.
12-SEP-1997; US-058785.
                       US-047615.
US-047617.
US-047612.
US-047633.
US-048964.
US-048964.
US-049610.
US-0591926.
US-055724.
US-056630.
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22-AUG-1997;
22-AUG-1997;
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22-AUG-1997;
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22-AUG-1997;
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06-JUN-1997;
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                                                                                                                        Disclosure; Columns 15-16; Zepp, English.

The present sequence encodes human bcl-y protein (Rbcl-y). The specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and Bcl-y are homologues of the bcl-2 protein thought to be involved in programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y contributions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in theraples to treat subjects suffering from: strokes, head trauma, larged in theraples to treat subjects suffering from: strokes, head trauma, larged in theraples to treat subjects suffering from: strokes, head trauma, larged in the cell death, aging, spinal cord injuries and amyotrophic lateral cell death, aging, spinal cord injuries and amyotrophic lateral cell death, aging, spinal cord injuries and amyotrophic lateral cell death as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, con extended period. In contrast, if they act as cell death stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and auco/hyperinmune diseases. They may also be used to cancer centered.
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                                                                                                 - useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.6%; Score 497.4; DB 1; Length 579; 91.2%; Pred. No. 1.2e-124; 1.1ve 0; Mismatches 51; Indels 0;
                                                                                            Novel bcl-y homologues of the rat and human bcl-2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                     111 T;
                                                                                                                                                                                                                                                                                                                                                                                                                 cause cell death in, and hence control, parasites. Sequence 579 BP; 106 A; 154 C; 208 G;
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                                                                                                              for modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               528; Conservative
11-FEB-1997; US-798897.
25-NOV-1997; US-978523.
                               (COCE-) COCENSYS INC.
                                                              WPI; 99-214150/18.
P-PSDB; W97392.
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Best Local Similarity
                                               Guastella J
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the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimune diseases, inflammatory diseases, various allergies, and as anti-infectious agents. The products can also be used for detection and diagnosis.
                                               20-NOV-1998 (first entry)
Nucleotide sequence of the cDNA clone Bcl-like (HAICH29).
Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction; immunological disorder; autoimmune disease; anti-infectious agent; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 12A-12D; 12Opp; English.
This is the nuclectide sequence of the CDNA clone Bcl-like (HAICH29), used in the method of the invention. The products of the clone can bused for treating conditions associated with abnormal expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cogotycaccaagccatgoggotyctggagacgaytttgagacccytttccgccgcacc 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies
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/product= "Bcl-like (HAICH29) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325 G;
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                                                                                                                                                                                                                                                                                                                                                                                                         21-JAN-1997; US-034204.
(AUCK-) AUCKLAND UNISERVICES LTD.
(HUMA-) HUMAN GENOME SCI INC.
Feng P, Gentz RL, Krissansen GW, Ni J, Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 5.2e-89,
0; Mismatches 42
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                                                                                                                                                                                         Location/Qualifiers
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V41925 standard; cDNA; 1098
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Best Local Similarity 90.3°
Matches 390; Conservative
                                                                                                                                                                                                                     .1098
                                                                                                                                                                                                                                                                                                                                                                                ; US-034205.
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P-PSDB; W59884.
                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-1997;
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O-MAY-1999 (first entry)

CDNA encoding the human bcl-y protein.

EAR bcl-y protein. Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; Rat bcl-y protein, Rbcl-y; human bcl-y protein; Brcl-y; bcl-z; brodramed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; premature cell death; cancer; premature cell death; cell death stimulator; prolonged cell life span; Raposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X15946 standard; cDNA; 579
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16-MAR-1999.
25-NOV-1997; 978523.
23-FEB-1996; US-012201.
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                                                                            Sequence
                                                                                                                   Query Match
                                                                                                                               Local
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                                                                                                                               Best Loca
Matches
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Claim 3: Column 15/16; 27pp; English.
The mammalian bcl-y genes encode a protein that is a member of the bcl-2
family, components in the cell death pathway. The bcl-2 family
                                                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                 360
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                                                                                                     61 aggetgaggeagaagggttatgtctgtggagetgggeetggggaaggeecageegeegae 120
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                           Gaps
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producing recombinant protein for use in treating uncontrolled cell
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ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
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                                                                caggtttccgacgaacttttccaagggggccctaactggggccgtcttgtgggcattcttt
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 Length 583;
                          Indels
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            Pred. No. 1.3e-125;
Score 501; DB
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                        0; Mismatches
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/product= bcl-y
/note= "No stop c
86.2%;
            91.48;
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V28334;
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                       Matches 531; Conservative
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23-FEB-1996; US-012201.
11-FEB-1997; US-798897.
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             Similarity
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P-PSDB; W61392.
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 Query Match
            Best Local
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have both apoptotic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired.
                                                                                                                                                                                                                                                                                                                                                                                                                       181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
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                                                                                                                                                                                                                           Length 579;
                                                                                                                                                  111 T;
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                        Score 497.4; DB 1;
Pred. No. 1.2e-124;
0; Mismatches 51;
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                                                                                                                                                  154 C;
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                                                                                                                                                                                                                        ch 85.6%; il Similarity 91.2%; 528; Conservative (
                                                                                                                                                  106 A;
                                                                                                                                                  579 BP;
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Claim 3; Page 48: 86pp; English.

This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene family, extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myozafula infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants.

Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis,
                                                                                                                                                                                                                                                                                                                                                           301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
                                                                        GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
                                                                                                                                                     caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacage 420
                                                                                                                                                                                                         421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg 480
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27-MAR-1996; AU-008965.
(AMRA-) AMRAD OPERATIONS PTY LTD.
Adams JM, Cory S, Gibson LM, Holmgreen SP;
WPI: 97-489635/45.
P-PSDB; W36647.
Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BCl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer; diagnosis; degenerative disease; ss.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody production or screening of potential modulators. Sequence 583 BP; 105 A; 157 C; 210 G; 111 T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .582
/*tag= a
/product= bcl-w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T96577 standard; DNA; 583 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human bcl-w DNA.
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An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w

Disclosure; Page 36; 52pp; English.

Disclosure; Page 36; 52pp; English.

The present sequence is described as a derivative of the human consent sequence is described as a derivative of the human color-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility of male animals. Methods are provided for the treatment of infertility, an animal model carries a mutation is at least one allele of the human or murine bcl-w gene con in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination.

They can be used to screen for therapeutes including
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181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
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Human bcl-w gene derivative.
Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
                                                                                                                                                                                                               caggittccgacgaactittccaagggggccctaactggggccgtcttgtggcatictit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce
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16-SEP-1997; AU-009228.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Adams J, COLY S, Gibson L, Koentgen F, Print C;
WPI; 99-243890/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 C;
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infertility.
583 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 animal model; ss.
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Novel Dcl.y nomologues of clil death number of process.

for modulating programmed cell death bisclosure; Columns 13-16; 26pp; English.

Disclosure; Columns 13-16; 26pp; English.

The present sequence encodes rat bcl.y protein (Rbcl.y). The sequence encodes rat bcl.y protein (Rbcl.y). Rbcl.y and Bbcl.y are homologues of the bcl.2 protein thought to be involved in Bbcl.y are homologues of the bcl.2 protein thought to be involved in Bbcl.y are homologues of the bcl.2 protein thought to be involved in Bbcl.y and Bb
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aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel bc1-y homologues of the rat and human bc1-2 protein - useful
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                                                                                                                                                                                                                                                                         23-FEB-1996; US-012201.
11-FEB-1997; US-798897.
25-NOV-1997; US-978523.
                                                                                                                                                                                                                                                                                                                                                                                 (COCE-) COCENSYS INC.
                                                                                                                                                                                                                                                 25-NOV-1997; 978523.
                                                                                                                                                                                                                                                                                                                                                                                                                                               99-214150/18.
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                                                                                                                        parasite; ss.
                                                                                                                                                                                                                  16-MAR-1999.
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Best Local Si
Matches 555;
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protein associated with Bol-w

protein associated with Bol-w

Claim 3; Page 32: 52pp; English.

Claim 3; Page 32: 52pp; English.

Claim 3; Page 32: 52pp; English.

The present sequence is the human bcl-w gene encoding Bcl-w protein

The present sequence is the human bcl-w gene encoding Bcl-w protein

The present sequence is the human bcl-w gene encoding Bcl-w protein

The present sequence is sesential for spermatogenesis. The widely expressed and which is essential for secules and genetic

The invention relates generally to a method of treatment and to an invention relates generally to a method of treatment of infertility, or animals. Methods are provided for the treatment of infertility, or animals. Methods are provided for the treatment of infertility, or animals. Methods are provided for the treatment of infertility, or model carries a mutation is at least one allele of the human or model carries a mutation is at least one allele of the human or model carries deminiferous tubules and are substantially infertille, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of the canimals, or which can induce infertility.

Sequence 581 Bp; 104 A; 155 C; 210 G; 112 T;
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                                     481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg 540
                                                                           481 cercrecescadescadacrescarcasreascadacasrescasses considerates care 540
421 AGTGGGGGCTGGGCCGAGTTCACAGCTCTATACGGGACGGGCCCCTGGAGGAGGACGC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An animal model exhibiting reduced levels of a Bcl-w protein and/or
                                                                                                                                                                                                                                                                                                                             Human bcl-w gene.
Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 86.5%; Score 502.6; DB 1; Length 581; Best Local Similarity 91.6%; Pred. No. 5e-126; Matches 532; Conservative 0; Mismatches 49; Indels 0;
                                                                                                                    541 gggccctggtaactgtagggcctttttgctagcaag 579
                                                                                                                                                            541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                     16-SEP-1997; AU-009228.
16-SEP-1997; AU-009228.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Adams J. COTY S, Gibson L, Koentgen F, Print C;
Mall: 99-243890/20.
                                                                                                                                                                                                                                                              X25132 standard; DNA; 581 BP.
                                                                                                                                                                                                                                                                                                        05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                    animal model; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; X05530
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-1999.
                                                                                                                                                                                                                                                                                         X25132;
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                                                                                                                                                                                                                                                                                                                ccyctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
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                                                                                                                                                                                             1 atgccgaccccagcctcaacccccagacacacgcgctctagtggctgactttgtaggctat 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacggggggccgtggcactg 540
                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                              481 cercrecegeageaacrececarcaereacacacacrecreacegeeccereecare 540
have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in sequence 581 BP: 106 A: 158 C: 200 G; 117 T;
                                                                                                                                                                                                                                                                                                                                                                                       caggtttccgacgaacttttccaagggggccctaactggggccgtcttgtggcattcttt
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGTTTCCGACGAACTTTTCCAAGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat bcl-y gene,
ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
                                                                                                                                     96.4%; Score 560.2; DB 1; Length 581; 97.8%; Pred. No. 1.8e-141; ative 0; Mismatches 13; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541 ggggccctggtaactgtaggggccttttttgctagcaagtg 581
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                                                                                                                                                                Matches 568; Conservative
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                                                                                                                                                   Local Similarity
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11-FEB-1997, 798897,
23-FEB-1996; US-0122
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growth e.g. cancers

Claim 2; Column 13/14; 27pp; English.

The mammalian bcl. y genes encode a protein that is a member of the bcl-2
family, components in the cell death pathway. The bcl-2 family,
have both apoptotic activity and the apoptosis blocking activity, bcl-y
falls in the apoptosis activity category. The recombinant protein may
be used to prevent uncontrolled cell growth, either by its direct
administration to recombinant genetic constructs to increase its
expression in vivo. Also, antisense constructs can be used in disorders
where prevention of cell death is desired.

Sequence 579 BP; 111 A; 157 C; 198 G; 113 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding the rat bc1-y protein.

Rat bc1-y protein; Rbc1-y; human bc1-y protein; Hbc1-y; bc1-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death;
                                                                                                                                                                                                                                                                                                                                                                                                                                           61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                               cogotgoaccaagocatgoggotgotgagacgagtttgagaccogtttccgccgcacc 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 agiggeggetgggeggacticacagetetatacggggaegggeeetggaggaegeaegg 480
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                                                                                                                                                                                                                                                                                                                                                                       421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGACGGGGCCCTGGAGGAGGCACGG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG 540
                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                         93.0%; Score 540.6; DB 1; Length 579; 95.9%; Pred. No. 3.2e-136; Live 0; Mismatches 24; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 ggggccctggtaactgtaggggcctttttgctagcaag 579
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            WPI; 98-446079/38.
P-PSDB; W61391.
                                                                                                                                                                                                                                                                                                                       3est_Local Similarity
Guastella J;
                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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Disclosure; Page 38; 52pp; English.

The present sequence is described as a derivative of the mouse of the present sequence is described as a derivative of the mouse of the present sequence is described as a derivative of the mouse of the pro-survival member of the Bol-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates of generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene cor in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including
                                                                                                                                                                                                                                                                                                                                                         540
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                                                                                                                                                                 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X25135;
05-JUL-1999 (first entry)
Mouse bcl-w gene derivative.
Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
                                                                                                                                gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga
181 TICICTETGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTCACC
                                                                                                                                                                                                                                                                                                                                                           cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg
                                                                                          CAGGITICCGACGAACITITCCAAGGGGGCCCTAACIGGGGCCGICIIGIGGCATICITI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTTGCTAGCAAGTG 581
                                                                                                                                                                                                                                                                                                                                                                                                                                  541 ggggccctggtaactgtaggggccttttttgctagcaagtg 581
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(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Adams J. Cory S, Gibson L, Koentgen F, Print C;
P-PSDB; Y05533.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X25135 standard; DNA; 581 BP.
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Score 581; DB 1; Length 581; Pred. No. 4.7e-147;

100.0%; 100.0%;

Query Match Best Local Similarity

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361 CAAGICCAGGATIGGAICGIGGCCIACCIGGAGACACGICIGGCIGACIGGAICCACAGG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 agtggcggctgggcggacttcacagctctatacggggacggggcctggaggacgcacgg 480
                                                                                                                                                     421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGACGCACGG 480
                                                                                           61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTGGGGAAGGCCCAGCCGCCGAC 120
                                                                                                                                                                                                                     ttetetgacetggeegeteagetacaegtgaceceaggeteageecageaaegetteace 240
                                                                                                                                                                                                                                                                                241 caggittccgacgaactittccaagggggccctaactggggccgictigtggcatictit 300
                           0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w Claim 3; Page 34; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse bcl-w gene.
Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                           caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc
                                                                                                                                                                                                                                       Indels
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16-SEP-1998; AU0764.
16-SEP-1997; AU-009228.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Adms J, Cory S, Gibson L, Koentgen F, Print (WPI; 99-243890/20.
   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X25133 standard; DNA; 581 BP
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    Matches 581; Conservative
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WO9913710-A1.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

(without alignments) 1263.465 Million cell updates/sec July 4, 2000, 01:26:24; Search time 115.05 Seconds Run on:

US-09-155-327B-8 581 Perfect score: Title:

1 atgeegaeeecageeteaae......geetttttgetageaagtg 581 Sequence:

311585 seqs, 125096042 residues Searched:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Scoring table:

623170 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

N\_Geneseq\_36:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|             | Description | Mouse bcl-w DNA. N | Mouse bcl-w qene d | 3      | Rat bcl-y gene. Nu |        | Human bcl-w gene. | Human bcl-w DNA. N |        | Human bcl-y gene. | cDNA encoding the | Nucleotide sequenc | Human secreted pro | Human thymus BCL-X | Bcl-XL gene. Induc | Base sequence of t | Bcl-2. Treating tu | Bcl-2 DNA fragment | Human oncogene bcl | Human bcl-2 gene. | Sequence of bcl-2 | Base sequence of t | Human BCL2 cDNA. S | Chicken lymphoid B | Human bcl-2 gene 0 | -ouco  | Sequence of bcl-2 | Mouse BCL-x gamma | Human thymus BCL-X | Human Cdn-3 DNA, N | Human Bax protein | cDNA encoding a hu | Bax omega protein | Bak-2 gene. Screen | Human Cdn-2 DNA. N |
|-------------|-------------|--------------------|--------------------|--------|--------------------|--------|-------------------|--------------------|--------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|-------------------|-------------------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|
|             | QI          | T96578             | X25135             | X25133 | 728333             | X15945 | X25132            | T96577             | X25134 | /28334            | X15946            | V41925             | 759630             | 181698             | T40079             | <b>K33182</b>      | 149815             | (33183             | 054631             | Q86661            | N81292            | 33184              | 133694             | 181696             | 073987             | X08431 | 181293            | V17638            | 181699             | Q95494             | 097606            | V84005             | 848               | T42139             | 095493             |
|             | DB ]        | -                  |                    |        |                    |        |                   |                    |        |                   |                   |                    |                    |                    | -                  |                    |                    |                    |                    |                   |                   |                    |                    |                    |                    |        |                   |                   |                    |                    |                   |                    |                   |                    |                    |
|             | Length      | 581                | 581                | 581    | 579                | 579    | 581               | 583                | 583    | 579               | 579               | 1098               | 1864               | 956                | 926                | 7372               | 765                | 953                | 5086               | 5086              | 5105              | 7996               | 760                | 1274               | 615                | 911    | 831               | 1384              | 737                | 5408               | 624               | 624                | 822               | 1286               | 6511               |
| ap (        | Match       | 0                  | 100.0              | 96.4   | 93.0               | 93.0   | 86.5              | 86.2               | 86.2   | 85.6              | 85.6              | 62.8               | 62.7               | 23.5               | 23.2               | 23.5               | 21.5               | 21.5               | 21.5               | 21.5              | 21.5              | 21.5               | 21.2               | 20.7               | 20.2               | 20.5   | 19.9              | 19.6              | 9.8                | 7.6                | 7.0               | 7.0                | 6.8               | 6.5                | 6.5                |
|             | Score       | 581                | 581                | 560.2  | 540.6              | 540.6  | 502.6             | 501                | 501    | 97.               | 97.               | 9                  | 6                  | 34                 | 134.6              | 34                 | 125                | 125                | 125                | 125               | 125               | 125                | 123.4              |                    | 119                | 11     | 115.8             | 13.               | 57                 | 4                  | ö                 | 。                  | 39.4              | ۲.                 | 37.6               |
| 1 1 1 1 1 1 | NO.         |                    | 7                  | m      | 4                  | S      | 9                 | 7                  | 80     | 6                 | 10                | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19                | 20                | 21                 | 22                 | 23                 | 24                 | 25     | 56                | 27                | 28                 | 53                 | 30                | 31                 | 32                | 33                 | 34                 |

| P.denitrificans ge<br>Bcl-Y cDNA. New is | Human Cdn-1 cDNA.<br>Bak gene. Screenin | Bak CDNA. New Bak- | Mycobacterium tube | M. tuberculosis im<br>BSSL/CEL Gene. DNA | Human adenosine Al | M. tuberculosis an |
|--|---|--------------------|--------------------|--|--------------------|--------------------|
| Q13287<br>T17375                         | Q95492<br>T42138                        | V61498             | V44433             | V64542<br>Q54222                         | X53491             | x01131             |
| н н                                      |   | ٦.                 |                    |  | Н                  | -                  |
| 3855<br>1968                             | 2072<br>2094                            | 2094               | 494                | 494<br>11531                             | 114955             | 496                |
| 6.4                                      | 6.3                                     | 6.3                | 9.0                | v. v.                                    | 5.8                | 5.8                |
| 37<br>36.4                               | 36.4<br>36.4                            | 36.4               | 34.4               | 33.8                                     | 33.8               | 33.6               |
| 35<br>36                                 | 37<br>38                                | 30                 | 4.1                | 4 4 2 2                                  | 44                 | 42                 |
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## ALIGNMENTS

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Nucleic acid encoding apoptosis related gene bcl-w - used to induce provided acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and degenerative diseases.

Claim 3: Page 50-51; 86pp; English.

This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene can mily. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, bypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell ines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                          Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer; diagnosis; degenerative disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 G;
                                                                                                                                                                                                                                                                                            (AMRA-) AMRAD OPERATIONS PTY LTD. Adams JW. Cory S, Glbson LM, Holmgreen SP; WPI; 97-489635/45. P-PSDB; W36048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 C;
                                                                                                                                              Location/Qualifiers
1..507
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/*tag= a
/product= bcl-w
/note= "q"
                              T96578 standard; DNA; 581 BP
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                                                           22-APR-1998 (first entry)
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27-MAR-1997; AU0199.
27-MAR-1996; AU-008965.
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                                                                               Mouse bcl-w DNA.
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Best Local
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This protein may be expressed recombinantly, particularly with porphasmids as vectors for expression in mammalian cell cultures. The protein has particular application in cancer cells (failure of programmed cell death (PCD)) or neurodegenerative and autoimmune diseases (premature PCD), e.g. Parkinson's disease, amylotrophic literature of the programmed cell death (PCD) and protein has particular application in cancer cells (failure of programmed cell death (PCD), e.g. Parkinson's disease, amylotrophic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-1996;
04-MAY-1995;
07-JUN-1995;
T-lymphocytes against cell death. A splice variant form, bol-xs, lacks a stretch of 63 amino acids, and is a dominant negative regulator of bcl-XL function. The gene may be modified to facilitate interaction with costimulatory Bax protein and inhibit interaction with antagonistic Bad protein, by modification of the Bcl-2 homology domains BH1 and/or BH2. The bcl-XL gene may be ector for HIV infection gene therapy, to augment intracellular a vector for HIV infection gene therapy, to augment intracellular bcl-XL protein levels and protect from cell death. A corresponding antisense oligonucleotide or expression vector may be used in gene therapy of e.g. autoimmune disease, graft rejection or graftversus-host disease, to induce cell death (e.g. apoptosis) and
                                                                                                                                                                                                                                                   Inducing or preventing death of T cells by bcl-XL protein regulation used to increase survival of HIV infected cells or to down:regulate immune responses in immune diseases Disclosure; Page 52-53; 76pp; English.

This is the sequence of a human bcl-XL protein, which protects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; Q81698.
                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; bcl-XL; T-lymphocyte; cell death; btl domain; bcl-XL; T-lymphocyte; cell death; btl domain; bcl-2 homology domain; gene therapy; HIV; AIDS; antisense; immune disorder; autoimmune disease; graft rejection; graft-versus-host disease; apoptosis; adoptive immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bcl-XL protein.
Human; bcl-XL; T-lymphocyte; cell death; BH1 domain; BH2 domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                               N-PSDB; T40079
                                                                                                                                                                                                                                                                                                                                                                                                                     04-MAY-1995; US-435518.
07-JUN-1995; US-481739.
(ARCH-) ARCH DEV CORP.
(USNA) US SEC OF NAVY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9634956-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 RLREG-N-WASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 KGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVKQALREAGDEFELRYRRAFSDLTSOLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
                                                                                                                                                                                                                                                                                                                                                                                CH, Thompson CB; 96-506159/50.
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77; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "BH1 domain"
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Pred. No. 7.90e-47;
30; Mismatches 36
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                                                                               145
                          205
                                                    101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160
                                                                                                                                                        Local Similarity 53.1%;
hes 77; Conservative
161 RLREG-N-WASVRTVLTGAVALGAL 183
                                                                                                                                   85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
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                                                                              SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
                                                                                                           KGQERFNRWFLTGMTVAGVVLLGSL 229
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pred. No. 7.90e-47;
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Search completed: Fri Jun 23 14:13:45 2000 Job time: 14 secs.

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claim 6; Page 50-51; 86pp; English.

This sequence represents a novel protein, bcl-w, encoded by the mouse bcl-2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to explants abundanted in phytidomas and to increases survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or
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                                                                                                                                                                                                                                                                                                                  61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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                                                                                                                                                                                                                                                                                                                                                                                               121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVAL 179
                                                                                                                                                                                                                                                                                                                                                                                                                    1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MATPASAPDTRALVADFVGYKLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                      1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
              substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.
                                                                                                                                                                                                                                                                            1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
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                                                                                                                                                       Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding apoptosis related gene bcl-w - used tor inhibit cell survival, e.g. for treatment of cancer and
Such animals have disorganised seminferous tubules and are
                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1202; DB 1; L
Pred. No. 3.67e-104;
8; Mismatches 1;
                                                                                                                                                           Score 1331; DB 1; 1
Pred. No. 6.54e-117;
                                                                                                                                                                                                   9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMRA-) AMRAD OPERATIONS PTY LTD.
Adams JM, Cory S, Gibson LM, Holmgreen SP;
WPI; 97-489635/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screening of potential modulators.
Sequence 168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W36048 standard; Protein; 168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis; degenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 86.0%;
al Similarity 94.6%;
159; Conservative
                                                                                                                                                           95.3%;
93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-APR-1998 (first entry)
                                                                                                                                                                              Best Local Similarity 93.8%;
Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-1997; AU0199.
27-MAR-1996; AU-008965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 GALVTVGAFFASK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse bcl-w protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; T96578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9735971-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                         Sequence
                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W36048;
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    888888888
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the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, various allergies, and as anti-infectious agents. The products can also be used for detection and diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 12A-12D; 120pp; English.
This is the amino acid sequence of the cDNA clone Bcl-like (HAICH29), used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCL-XL; apoptosis; cell death; cancer; neurodegenerative disease; autoimmune disease; Parkinson disease; amylotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFELGAALCAESVNKEWEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                            20-NOV-1998 (first entry)
Amino acid sequence of the cDNA clone Bcl-like (HAICH29).
Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction; immunological disorder; auttoimmune disease; anti-infectious agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotides and encoded polypeptides - used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 75.1%; Score 1049; DB 1; Length 365; Local Similarity 98.6%; Pred. No. 4.39e-89; hes 142; Conservative 1; Mismatches 1; Indels
121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA 168
                    121 QVQEWMVAYLETRLVDMIHSSGGWAEFTALYGDGALEEARRLREGNWA 168
                                                                                                                                                                                                                                                 23-JUL-1998.
21-JAN-1998; U00960.
21-JAN-1997; US-034205.
21-JAN-1997; US-034204.
340CK-) AUCKLAND UNISERVICES LTD.
(HUMA-) HUMAN GENOME SCI INC.
Feng P, Gentz RL, Krissansen GW, Ni J, Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 QVQEWMVAYLETRLADWIHSSGGW 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 QVQEWMVAYLETRLVDWIHSSGGW 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R68887 standard; Protein; 233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nunez G, Thompson CB;
                                                                                           T 13
W59884 standard; Protein; 365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JAN-1995.
22-JUN-1994; U07089.
22-JUN-1993; US-081448.
(ARCH-) ARCH DEV CORP.
(UNMI ) UNIV MICHIGAN.
Boise LH, Nunez G, Thon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human thymus BCL-XL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  98-414099/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
WO9500642-A.
                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 98-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R68887;
                                                                                                                               W59884;
                                                                                                                                                                                                                                                                                                                                                                                   Su JY;
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for modulating programmed cell death

Claim 2: Columns 19-22: 26pp; English.

The present sequence represents a mammalian bcy-1 protein.

The present sequence represents a mammalian bcy-1 protein.

The present sequence represents a mammalian bcy-1 protein.

The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y

protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein

thought to be involved in programmed cell death (apoptosis and necrosis).

Rbcl-y and Hbcl-y proteins may be used to treat conditions associated

with a disruption of the cell death pathway. If they act as cell death

thought to be used in themspies to treat subjects suffering

from: strokes, head trauma, Alzheimer's Disease, neural and muscular

degenerative diseases (especially multiple sclerosis), myocardial

infarction, vitally induced cell death, ading, spinal cord injuries and

amyotrophic lateral sclerosis- conditions where cells under go premature

cell death as a result of triggers which may or may not be apparent.

They may also be used on extended period. In contrast, if they act as

cell death stimulators, Rbcl-y and Hbcl-y may be used to treat

conditions associated with prolonged cell life span such as cancer

conditions associated with prolonged cell life span such as cancer

conditions associated with prolonged cell life span such as cancer

conditions associated with prolonged cell life span such as cancer

conditions associated with prolonged cell life span such as cancer

conditions associated with prolonged cell life span such as cancer

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conditions as cancer and cell place and cell life span and cell shall man and contract as cancer.
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Protein sequence of the specification.

Protein sequence of the specification.

Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; head trauma; sclenosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Raposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                  Novel bcl-y homologues of the rat and human bcl-2 protein - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 99\text{-}214150/18. Novel bcl-Y homologues of the rat and human bcl-2 protein - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
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Pred. No. 1.42e-120;
1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 98.4%;
Matches 189; Conservative
25-NOV-1997; US-978523.
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23-FEB-1996; US-012201.
11-FEB-1997; US-798897.
25-NOV-1997; US-978523.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 ALVIVGAFFASK 193
                         (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (COCE-) COCENSYS INC. Guastella J;
                                                                              99-214150/18.
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16-MAR-1999.
                                                  Guastella J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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for modulating programmed cell death

Disclosure; Columns 19-20; 26pp; English.

The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
protein (Hbcl-y). Rbcl-y and Hbcl-y proteins of the bcl-2 protein

thought to be involved in programmed cell death (apoptosis and necrosis).

CR Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
with a disruption of the cell death pathway. If they associated
with a disruption of the cell death pathway. If they associated
with a disruption of the cell death pathway. If they act as cell death
inhibitors, they may be used in therapies to treat subjects suffering
from: strokes, head trauma, Alzheimer's Disease, neural and muscular
degenerative diseases (especially multiple sclerosis), myocardial
infarction, vitally induced cell death, aging, spinal cord injuries and
amyotrophic lateral sclerosis- conditions where cells under go premature
cell death as a result of triggers which may or may not be apparent.
They may also be used in this way to develop cell lines which remain
viable in culture for an extended period. In contrast, if they act as
coll death stimulators, Rbcl-y and Hbcl-y may be used to treat
(especially kaposi's sarcoma and lung canneer) and auto/hyperimmune
conditions associated with prolonged cell life span such as cancer
diseases. They may also be used to cause cell death in, and hence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein associated with Bcl.w

Disclosure; Page 39; 52pp; English.

The present sequence is described of a derivative of mouse Bcl-w
(see also 905531), a pro-survival member of the Bcl-2 family that
is widely expressed and which is essential for spermatogenesis.

The derivative lacks the 24 N-terminal amino acids of Bcl-w.

The invention relates generally to a method of treatment and to an
animal model for the identification of molecules and genetic
sequences useful for inducing or reducing fertility of male animals.

Methods are provided for the treatment of infertility, or for
Rethods are provided for the treatment of infertility, or for
reducing fertility, by modulating spermatogenesis. An animal model
carries a mutation is at least one allele of the human or murine
bcl-w gene (see X25132-35) or in a gene associated with bcl-w.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATPASTPDTRALVADEVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An animal model exhibiting reduced levels of a Bcl-w protein and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ATPASAPDTRALVADFVGYKLROKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1367; DB 1; Pred. No. 1.79e-120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-1999 (first entry)
Mouse Bcl-w protein deritvative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5,,....
Best Local Similarity 97.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-SEP-1998; AU0764.
16-SEP-1997; AU-009228.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          control, parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; X25135
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181 GALVTVGAFFASK 193

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RESULT
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The present sequence represents rat bcl-y protein (Rbcl-y). The specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and bcl-y are homologues of the bcl-2 protein thought to be involved in programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y corpresents are conditions associated with a disruption of programmed cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, and in therapies to treat subjects suffering from: strokes, head trauma, cell death, aging, spinal cond injuries and amyotrophic lateral cell death, aging, spinal cord injuries and amyotrophic lateral cell death, aging, spinal cord injuries and amyotrophic lateral solerosis conditions where cells under go premature cell death as a cell death as to extended period. In contrast, if they act as cell death stimulators, an extended period. In contrast, if they act as cell death stimulators, colonged cell life span such as cancer (especially kaposi's sarcoma and control, parasites.
                                                                                                                                                                                                   The rat bc1-y protein.

The rat bc1-y protein.

Rat bc1-y protein, Rbc1-y; human bc1-y protein; Hbc1-y; bc1-2 homologue; Rat bc1-y protein; Rbc1-y; human bc1-y protein; Bc1-y protein; Bc2-y protein; Bc2-y protein; Bc2-y; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; adjudy; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel bcl-y homologues of the rat and human bcl-2 protein - useful for modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1378; DB 1; Length 193; Pred. No. 1.46e-121;
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                                                                                                                                                     W97391 standard; Protein; 193 AA.
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Best Local Similarity 97.4%;
watches 18%; Conservative
                                                                                                                                                                                     20-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       25-NOV-1997; 978523.
23-FEB-1996; US-012201.
11-FEB-1997; US-798897.
25-NOV-1997; US-978523.
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                                                    181 GALVTVGAFFASK 193
                                                                                      181 GALVTVGAFFASK 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 AA;
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                                                                                                                                                                                                                                                                                                                                                           Rattus sp.
US5883229-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guastella J;
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                                                                                                                                                                       W97391;
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                                                                                                                                         RESULT
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Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The mammalian bolly protein is a member of the boll-2 family, components in the cell death pathway. The boll-2 family have both apoptotic activity and the apoptosis blocking activity. bolly falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FSDLAAQLHVIPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell growth e.g. cancers
                                                                                           Rat bcl-y protein.
bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1378; DB 1; Length 193;
Pred. No. 1.46e-121;
4; Mismatches 1; Indels (
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.T 8
W61391 standard; Protein; 193 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Fig 3A; 27pp; English.
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Best Local Similarity 97.4%;
Matches 188; Conservative
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                                                                   02-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalian bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-012201.
US-798897.
                                                                                                                                                                                                      11-FEB-1997; 798897.
23-FEB-1996; US-012201.
11-FEB-1997; US-798897.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            death is desired.
Sequence 193 AA;
                                                                                                                                                                                                                                                                                                                       WPI; 98-446079/38.
                                                                                                                                                                                                                                                                                                                                                N-PSDB; V283333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAR-1999.
25-NOV-1997; 9
23-FEB-1996; U
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                                                                                                                                                             US5789201-A.
                                                                                                                                                                                     04-AUG-1998.
                                                                                                                                                                                                                                                                                                    Guastella J;
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                                                                                                                                       Rattus sp.
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                                                W61391;
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growth e.g. cancers

Example. Column 17/18: 27pp; English.

The mammalian bcl.y protein is a member of the bcl.2 family, components in the cell death pathway. The bcl.2 family have both apoptotic activity and the apoptosis blocking activity. bcl.y falls in the apoptosis activity activity activity activity activity ategory. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to antisense constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired.
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                                                                                                                                                                                                                                                                                                                                                   1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                 fertility of male animals. Wethods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene (see X25132-35) or in a gene associated with bcl-w. Such animals have disorganised seem inferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapentic molecules including qenetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; V28334.
Nucleic acids encoding B-cell lymphoma-y protein - useful for
producing recombinant protein for use in treating uncontrolled cell
molecules and genetic sequences useful for inducing or reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human bcl-y protein.
bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
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0
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Pred. No. 1.16e-121;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                              3; Mismatches
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98.48;
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                                                                                                                                                                                                                                                                         Local Similarity 97.9%;
les 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-FEB-1996; US-012201.
11-FEB-1997; US-798897.
(COCE-) COCENSYS INC.
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                                                                                                                                                                                                                      193 AA;
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                                                                                                                                                                                                   Infertility
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                                                                                                                                                                                                                                                        Query Match
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Matches
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The property of the part and numan bol-2 protein - useful.

The modulating programmed cell death

Cor modulating based but a bol-3 protein (Rbol-y). The

Specification also describes rat bol-y protein (Rbol-y). Rbol-y and

Bbol-y are homologues of the bol-2 protein thought to be involved in

Corporammed cell death (apoptosis and necrosis). Rbol-y and Hbol-y

Corporammed cell death pathway. If they act as cell death inhibitors, they may be

Corporating may be used to treat conditions associated with a disruption of

Corporation also treat the pathway of they act as cell death inhibitors, they may be

Coursed in therapies to treat subjects suffering from: strokes, head trauma,

Alzheimer's Disease, neural and muscular degenerative diseases

Coll death, aging, spinal cord injuries and amyotrophic lateral

sclerosis-conditions where cells under go premature cell death as a

cell death, aging, spinal cord injuries and amyotrophic lateral

sclerosis-conditions where cells under go premature cell death as a

cell death, aging spinal cord injuries and myotrophic lateral

sclerosis-conditions where cells in they act as cell death stimulators,

Coused in this way to develop cell life where conditions associated with

Rbol-y and Hbol-y may be used to treat conditions associated with

Couse cell death sim, and hence control, parasites.
                                                                                                                                                                                                                                                                                                                                                              The human bolyprotein.

The human bolyprotein.

Rat boly protein, Rboly, human bolyprotein; Hboly; boll-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple solerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premarure cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
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                  OVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                          FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel bcl-y homologues of the rat and human bcl-2 protein - useful
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Pred. No. 1.16e-121;
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98.48;
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11-FEB-1997; US-798897.
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                                                                                                                                                                                              GALVTVGAFFASK 193
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25-NOV-1997; 978523.
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US5883229-A.
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121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

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Gaps

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2; Indels

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1 MATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60 

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N-PSDB; X25133
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WO9913710-A1.
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W09913710-A1
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                        25-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or inhibit cell survival, e.g. for treatment of cancer and degenerative diseases
claim 6; page 48 86pp; English.
This sequence represents a novel human protein, bcl-w, encoded by the bcl-2 gene family and extracted from an adult brain library. This gene promotes cell survival, so its modilation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, alzhehmer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential modulators.
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                                                                      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120
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                                                                                                                                                                                                                                                                                                                                                     Human bcl-w protein.
Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
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Pred. No. 1.91e-123;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMRA-) AMRAD OPERATIONS PTY LTD.
Adams JM, Cory S, Gibson LM, Holmgreen SP;
WPI; 97-489635/45.
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Y05530;
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W36O47 standard; Protein; 193 AA.
                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis; degenerative disease
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nes 193; Conservative
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27-MAR-1996; AU-008965.
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Matches
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In the sociated with BCl-w

Trotein associated with BCl-w

Trotein associated with BCl-w

Trotein associated with BCl-w

Staim 21, Page 31, 55pp. English.

The present sequence is human BCl-w, a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing a fertility of male animals. Methods are provided for the treatment.

Spermatogenesis. An animal model carries a mutation is at least of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least of a sensociated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no cher major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise infinity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein associated with Bcl-w
Claim 2; Page 35; 52pp; English.
The present sequence is mouse Bcl-w, a pro-survival member of the
Bcl-2 family which is widely expressed and which is essential for
spermatogenesis. The invention relates generally to a method of
treatment and to an animal model for the identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-1999 (first entry)
Mouse Bcl-w protein essential for spermatogenesis.
Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
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Pred. No. 4.66e-122;
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                                                                                                                Gibson L, Koentgen F, Print
16-SEP-1998; AU0764.
16-SEP-1997; AU-009228.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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ilarity 99.0%;
Conservative
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16-SEP-1997; AU-009228.
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Matches 191; Conser
                                                                                                                Adams J, Cory S, Gi
WPI; 99-243890/20.
N-PSDB; X25132.
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Jun 23 14:13:31 2000; MasPar time 7.29 Seconds 626.869 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-155-327B-7 (1-193) from US09155327B.pep 1397 Title: Description: Perfect Score: Sequence:

1 MATPASAPDTRALVADFVGY......LTGAVALGALVTVGAFFASK 193

PAM 150 Gap 11 Scoring table:

Post-processing:

188963 seqs, 23686106 residues

Searched:

Minimum Match 0% Listing first 45 summaries

1:geneseqp a-geneseq36 Database:

Mean 32.637; Variance 140.214; scale 0.233 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Pred. No.           | 1.91e-123<br>1.91e-123<br>4.26e-122<br>1.16e-121<br>1.46e-121<br>1.42e-121<br>1.42e-120<br>1.79e-120<br>1.39e-89<br>4.39e-47<br>7.90e-47<br>7.90e-47<br>7.90e-47<br>7.02e-43<br>7.02e-43  |  |
|---------------------|---|--|
| Description         | Human Bclw protein es Human bclw protein. Human bclw protein es Mouse Bclw protein es Human bcly protein. The human bcly protein. The human bcly protein. Rat bcly protein. Rat bcly protein. Rat bcly protein. Protein sequence of th Mouse Bclw protein de Mouse Bclw protein de Mouse Bclw protein. Amino acid sequence of Human thymus BclXL. BclXL. Human anti-apoptotic B. Poperenyl (RTM)-induc A. human Bcl2 protein. A. human Bcl2 alpha pr Human bcl2 |  |
| SUMMARIES           | Y05532<br>W36047<br>Y055310<br>W61392<br>W97392<br>W97393<br>W61391<br>W97394<br>W97393<br>Y05533<br>Y05533<br>W36048<br>W375048<br>W19396<br>W19396<br>W87812<br>W87812<br>W87812<br>W87812<br>W87812<br>W87812  |  |
| 80                  |   |  |
| Length DB           | 193<br>193<br>193<br>193<br>193<br>193<br>233<br>233<br>233<br>233<br>233<br>233<br>233<br>233<br>233   |  |
| %<br>Query<br>Match | 1000.0<br>989.0<br>988.0<br>988.7<br>988.7<br>988.7<br>98.7<br>997.9<br>98.6<br>98.7<br>98.7<br>98.7<br>98.7<br>98.7<br>98.7<br>98.7<br>98.7  |  |
| Score               | 1397<br>1397<br>1383<br>1388<br>1379<br>1378<br>1378<br>1378<br>1378<br>1368<br>1368<br>616<br>616<br>616<br>616<br>615<br>615<br>615<br>615<br>615<br>615  |  |
| Result<br>No.       | 22222222222222222222222222222222222222  |  |

| 7.02e-43<br>1.36e-42<br>1.36e-42<br>1.36e-42<br>1.36e-42<br>1.36e-42<br>1.36e-42<br>6.42e-42<br>6.42e-42<br>1.55e-41<br>3.12e-39   | 1.34e-35<br>1.34e-35<br>1.34e-35<br>1.34e-35<br>1.49e-35<br>9.46e-31<br>9.46e-31   |
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| Sequence of bc1-2-alph Human oncogene bc1-2 papotosis-blocking pro Human Bc1-2 mutant pro A murine Bc1-2 protein Human Bc1-2 valid-type Apoptosis-blocking pro Apoptosis-blocking pro Human Bc1.2 mutant pro Human Bc1.2 mutant pro Chicken lymphoid Bc1-X Mouse BC1-X gamma. Human thymus BC1-X | Human anti-apoptotic B A human Bcl-2-beta pro Human bcl-2 beta protein. Bcl-2 polypeptide. Sequence of bcl-2-beta Human Bcl-2 mutant pro Apoptosis-blocking pro Human thymus BCL-XI. |
| P80987<br>R47344<br>W01019<br>W34346<br>W34811<br>W94345<br>W01018<br>W01020<br>W94347<br>W02383<br>R68884<br>R68884   | W31529<br>W87813<br>R71405<br>R70332<br>W96319<br>P80988<br>W94348<br>W01021   |
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## ALIGNMENTS

ö Gaps Score 1397; DB 1; Length 193; Pred. No. 1.91e-123; 0; Mismatches 0; Indels 0; Query Match 100.0%; Best Local Similarity 100.0%; Matches 193; Conservative

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- 61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEDLVG 120 QY q

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662 GCATGACTCTAGCTGGGG 679

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161 agacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccaggct 220
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//b_xref="G1:998482"
/translation="PISITKMSQSNRELVVDFLSYKLSQKGYSWSQFSDVBENRTEAP
EETPERETPSAINGNPSWHLADSPAVNGATGHSSSLDAREVLPMAAVKQALREAGBE
FELRYREAFSDLTSOLHITPGTVYQSFEQVVWELFRDGVNWGRIVASSSFGGALCVES
VEKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNTAPESRKGQERFNR
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Tallly, J.L., Tilly, K.I., Kenton, M.L. and Johnson, A.L.

Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels Endocrinology 136 (1), 232-241 (1995)
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341 agatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgcggc 400
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                                                                                                                                                                                                                                                                                                                                26-SEP-1995
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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bcl-x=apoptosis inhibitor [protooncogene] [rats, ovary, mRNA
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VLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQERFNRWFLTGM
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Direct Submission
Submitted (13-DEC-1999) Biochemistry, SUNY at Buffalo, 3435 Main
Street, Buffalo, NY 14214-3000, USA
Location/Qualiflers
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Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 720)
Lee.T.L. and Canty,J.M.
PCR Cloning of a Porcine bcl-xL cDNA from Heart
                                                                   cageceageaacgettcaceceaggteteegaegaacttttteaagggggeeecaaetggg
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/db_xref="GI:6959767"
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/db_xref="taxon:9823"
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Lee, T.L. and Canty, J.M.
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DB 3; Length 720;

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REPEALNORMSWHLADSPANWGATGHSSLDAREVIPMAANYGALREAGDEFELRYR
RAFSDLTSQLHITPGTAYQSFBQVNRELFRDGVNWGRIVAFFSFGGALCVESVDKEWO
VLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESRKGGEFFNRWFLTGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation-"MSQSNQELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPE
RETPSAINGNPSWHLADSPAVNGATGHSSSLDAREVIPWAAVKQALREAGDEFELRYR
RAFSDLTSQLHITPGTAYQSFEQDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGV
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                                                                                                                                                                                    /tissue_type="brain"
/clone_lib="hippocampal cDNA libr. and genomic DNA libr."
/clone="X9, X31"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 agacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccaggct 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCGCATTGTGGCCTTCTTCTCTTTGGCGGGCCACTGTGCGTGGAAAGCGTAGAAGG 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="smaller form due to splicing"
                                                                                     /organism="Rattus norvegicus"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="SWISS-PROT:P53563"
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/db_xref="G1:607178"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAA57886.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(20. .394,584. .721)
/gene="bcl-x"
                                                                                                                                                    /dev_stage="embryonic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="GI:607177
                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                        /gene="bcl-x"
                                                                                                                                                                                                                                                                                                                                                                                                    /gene="bcl-x"
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BASE COUNT 47
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Tilly, J.L., Tilly, K.I., Kenton, M.L. and Johnson, A.L. Direct Submission

Direct Submission

Bubmitted (28-AUG-1995) Jonathan L. Tilly, Department of Obstetrics and Gynecology/Vincent Center for Reproductive Biology,

Massachusetts General Hospital/Harvard Medical School, 32 Fruit Street, Boston, MA 02114, USA

Location/Qualifiers
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RETPSAINORPSWHLADSPAVNGATCHSSSLDAREVLPMAAKQALREADERELRYR
RETPSAINORPSWHLADSPAVNGATCHSSSLDAREVLPMASKGALCVESVDKEMO
RLYSRIASWAATYLNDHLEPWIQENGGWDTFVDLYGNWTAPESRKGQERENRWFLTGM
                                                                                                                                                                                                                                                                                                                                                                            Eukaryotta, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.

1 (bases 1 to 726)

1 (111), J.L., Tilly, K.I., Kenton, M.L. and Johnson, A.L.
Expression of members of the bcl-2 gene family in the immature rat evary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels Endocrinology 136 (1), 232-241 (1995)
                                                                                                                                                      Rattus norvegicus programmed cell death repressor BCL-X-Long mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="programmed cell death repressor; Bcl-2 homolog; long isoform of BCL-X; member of the bcl-2 gene family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 agacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccaggct 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="BCL-X-Long"
/protein_id="AAA77686.1"
/db_xref="GI:1004377"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="ovary"
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672 TGACTGTGGCTGGTGTAGT 690
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ORIGIN
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/codon_start=1
/product="Bc1-x"
/product="Bc1-x"
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/db_xref="C1:505699"
/translation="MSOSNRELVUDSLSYKLSQKGYSWSQFSDVEBNRTEAPEETEPE
//translation="MSOSNRELVUDSLSYKLSQKGYSWSQFSDVEBNRTEAPEETEPE
//translation="MSOSNRELVUDSLSYKLSQKGYSWSQFSDVEBNRTEAPEETEPE
//translation="MSOSNRELVUDSLSYKLSQKGYSWSQFSDVEBNRTEAPEETERPE
//translation="MSOSNRELVUDSLSYKLSQKGYSWSQALCVESYDKEN
/VVSRIASWMATYLNDHLEPMIQENGGWDTFVDLYGNNAAABSSKKGQERFNRWFLTGM
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Shiraiwa, N., Inohara, N., Okada, S., Yuzaki, M., Shoji, S. and Ohta, S.
An additional form of rat Bcl-x, Bcl-xbeta, generated by an unspliced RNA, promotes apoptosis in promyeloid cells
J. Biol. Chem. 271 (22), 13258-13265 (1996)
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Shiratwa, N., Inohara, N., Okada, S., Yuzaki, M., Shoji, S. and Ohta, S.
Direct Submission
Birect Submission
Birect Submission
Of State of Secondary of Institute of Gerontology, 1-396 Kosugi-cho, Nakahara-ku, Kawasaki City 211, Japan
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Pred. No. 1.8e-22;
0; Mismatches 185; Indels
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Rattus norvegicus Bcl-xalpha mRNA, complete cds.
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Matches 254; Conservative
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RAFSDLTSQLHITPGTAYQSFEQVVNELFROGVNWGRIYAFFSFGGALCVESVDKEMO
VLVSRIASWAATYLNNHLEPWIQENGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGM
TVAGVVLLGSLFSRK"
                                                                                                                                                                                                                  /translation="mSQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPE
RETPSAINGNPSWHLADSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYR
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Rattus.
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Submitted (04-NOV-1994) T.M. Michaelidis, Max-Planck-Inst.
Submittery, Dept of Neurochemistry, 82152 Martinsried, FRG
2 (bases 1 to 2232)
Michaelidis, T.M.
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1 (bases 1 to 2232)
Michaelidis, T.M.
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Best Local Similarity 57.9%; Pred. No. 1.6e-22;
                           /organism="Rattus norvegicus"
/db_xref="taxon:10116"
72. .773
                                                                                                                                                                                                                                                                                                                                         381
                                                                                                                                        /product="Bc1-xalpha"
/protein_id="AAB17353.1"
/db_xref="G1:1622937"
Location/Qualifiers
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Rattus norvegicus
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Eutheria; Rodentia; 3
1 (bases 1 to 764)
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Hardwick, J.M.
 Conservative
 Matches 370;
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DLGSRALVEDLVRYKLCQRSLVPEPSGAASCALHSAMRAAGDEFEERFRQAFSEISTQ
IHVTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (02-NOV-1994) J.A. Cruz-Reyes, National Institute of
Medical Research, NIMR/MRC Mill Hill, The Ridgeway Road, London NW7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MVTYLETNLRDWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGAL.
MTVGALFASK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloning, characterization and expression of two Xenopus bcl-2-like cell-survival genes
Gene 158 (2), 171-179 (1995)
                              301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
                                                                     caggiciccgacgaactititicaagggggccccaactggggccgccttgtagccttcttt 300
                                                                                                                                                                                    caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Vertebrata; Amphibia; Batrachia;
Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                        01-JUL-1997
              181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 238.2; DB 4; Length 749;
Pred. No. 9.3e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. 749
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/db_xref="taxon:8355"
/dev_stage="28-30 (tailbud tadpole)"
/clone_lib="lambda ZapII:R1"
                                                                                                                                                                                                                                                                                                                                        VRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SWISS-PROT:091827"
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/db_xref="GI:1334682"
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3. .689
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                                                                                                                                                                                                                                                                                                                                     XLR1 749 bp
X.laevis R1 mRNA.
X82462
X82462.1 GI:575421
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3. .689
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African clawed frog.
Xenopus laevis
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Cruz-Reyes, J.A.
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VERSION
KEYWORDS
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TITLE
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Direct Submission
Submitted (13-JUN-1994) J. Marie Hardwick, Neurology, Johns Hopkins
School of Medicine, 600 North Wolfe St., Baltimore, MD 21287-7681,
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                                                                                                                                                                                                                                                     136 atgcgggcagctggagatgagttcgagacccgcttccggcgcaccttctctgatctggcg 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ctttttcaagggggccccaactggggccgcttgtagccttcttctcttttggggctgca 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             496 aactggggcatcagtgaggacagtgctgacgggggccgtggcactgggggccctggtaact 555
                                                                                                                                                                         192 AGTCTGGTTCCGGAGCCT-----TCAGGAGCAGCAGCATCCTGTGCTTTGCATTCGGCT 242
                                                                                                                                                                                                                                                                                             gotcagotgcatgtgaccccaggctcagcccagcaacgcttcacccaggtctccgacgaa 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 ctgtgtgctgagagtgtcaacaaggagatggaaccactggtgggacaagtgcaggagtgg 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 atggtggcctacctggagacgcggctggtcgactggatccacagcagtgggggctgggcg 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483 ATGGTGACATATCTGGAGACAAACCTGAGACTGGATTCAGAGCAATGGTGGCTGGAAT 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 gagttcacagctctatacggggacggggccctggaggaggcgcggcgtctgcgggagggg 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 TCTGACCTAGGATCCCGGGCTTTGGTAGAGGATTTGGTGAGGTACAAGTTATGCCAGCGT 191
                                                                                                                              76 ggttatgtctgtggagctggccccgggggagggcccagcagctgacccgctgcaccaagcc 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 ACACAGATCCATGTGACCCCCGGCACAGCATATGCACGCTTTGCAGAAGTAGCAGGTAGC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 CTATTCCAAGGFGGGGFGAAFFGGGGTCGCAFAGFTGCAFFTFTFTFFFFFFGFGCCGCG 422
16 tcggccccagacacacgggctctggtggcagactttgtaggttataagctgaggcagaag 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAUT10579 764 bp DNA ROD 24
Rattus norvegicus Bcl-x (bcl-x) gene, complete cds.
U10579
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1. .764
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39. .740
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/gene="bcl-x"

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/note="matching EMBL:AA452257; Identified using the e-PCR software (G. Schuler)"
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107753. .107946
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software (G. Schuler)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="matching EMBL: W78986; Identified using the e-PCR software (G. Schuler)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="matching EMBL:H72023; Identified using the e-PCR
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107991. .108176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="matching EMBL:R59134; Identified using the e-PCR
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                                                                                                                                                                                                                                                                                             /note="matching EMBL:D11677; Identified using the software (G. Schuler)" 128383. .128521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 423.4; DB 10; Length 196287;
Pred. No. 2.1e-85;
0; Mismatches 6; Indels 0; G
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software (G. Schuler)"
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                                                                                                                                                                                                                                                                                 /standard_name="D11677"
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Best Local Similarity 98.6%;
Matches 427; Conservative (
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ALO49829
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On Oct 28, 1999 this sequence version replaced gi:4972127.
IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the
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software (G. Schuler)"
80431. .80564
                                                                                                                                                                                                                                                 cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcatg 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                            agiggggctgggggggggttcacagctctatacggggacggggccctggaggaggcgcgg 480
                                                                                                                                                                                                                                                                                                                                                                                                                        caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
                                                                                                                                                                                                                                                                                                                                                           CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 598
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                        ttetetgatetggeggeteagetgeatgtgaececaggeteageceageaacgetteaee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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78257. 78396
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1. .196287
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Query Match
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                                                                                                                                                                                                                                                                                                                  /translation-"MATPASTPDTRALVADFVGYKLRQKGYVCGAGFGEGFAADPLHO
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RLREGSNRRASVRFYGAVLGALUZVTVGAFFASK"

1158 c 200 g 117 t
Gibson, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and
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                                          Submitted (03-JUN-1996) Molecular Biology Unit, The Walter ar
Eliza Hall Institute of Medical Research, Po Royal Melbourne
Hospital, Parkville, Victoria 3050, Australia
Location/Qualifiers
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                                                                                                                                                                                                                             /gene="bcl-w"
/note="promotes cell survival; Bcl-2 homolog"
/codon_start=1
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Best Local Similarity 93.6%; Pred. No. 2.4e-107
Matches 545; Conservative 0; Mismatches 37
                                                                                                                                                                                                                                                                         /product-"Bcl-w"
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1. .582
/gene="bcl-w"
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AMAAGDEFETRREREPSDLAAQLHYPGSAQQRFTQVSDELFQGGPRWGRLVAFFVP
GAALCAESWKEMEPLVGQVQDWMVAXLETRLADWIHSSGGWAEFTALYGDGALEBAR
RLREGNWASVRTVLTGANALCALVTVQCAFFASK"
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                                                                                                                                                 Eutheria; Rodentia; Solurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3476)
Ross,A.J., Waymire,K.G., Moss,J.E., Parlow,A.F., Russell,L.D. and
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                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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                                                                                                                                                                                                                                                          Chases 1 to 3476)
Ross, A.J. and MacGregor, G.R.
Direct Submission
Submitted (21-OCT-1997) Center for Molecular Medicine,
University, 1462 Clifton Road, Atlanta, GA 30322, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
 Mus musculus BCL-W (Bcl-w) mRNA, complete cds. AF030769
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0; Mismatches 37;
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Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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                                                      AF030769.1 GI:2623249
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3356. .3364
/gene="Bcl-w"
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RAALCAESVNKEMEFLAGVGALVYYGAFFASK"
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                                          /note="Bcl-2 family member"
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 1. .582
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Matches 548; Conservative
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Metazoa; Chordata; Ciurognathi; Muridae; Murinae; Mus.
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 582)
Gibson,L., Holmgreen,S.P., Huang,D.C.; Bernard,O., Copeland,N.G., Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S. bcl-w, a novel member of the bcl-2 family, promotes cell survival 96358615
2 (bases 1 to 582)
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                        homologue
                                                                                                                                                                                                                 0; Mismatches
Guastella,J.
Genes coding for bcl-y a bcl-2 homo
Patent: US 5789201-A 1 04-AUG-1998;
Location/Qualifiers
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                                                                                          /organism="unknown"
157 c 198 g
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Best Local Similarity 94.0%;
Matches 544; Conservative
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AMRAAGDEFETRFRRFSDLAAQLHVTPGSAQORFTQVSDELFQGGPNWGRLVAFFVF
RAALCABSVRKEMEPLVGQVQEWNVXLETRLADWIHSSGGRAEFTALYGDGALEEAR
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                                                              Query Match 98.6%; Score 575; DB 9; Length 35
Best Local Similarity 99.1%; Pred. No. 4.2e-119;
Matches 578; Conservative 0; Mismatches 5; Indels
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Patent: US 5789201-A 2 04-AUG-1998
Location/Qualifiers
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Guastella, J.
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Hamner,S., Skoglosa,Y. and Lindholm,D.
Differential expression of Bcl-w and Bcl-x mRNA in the developing
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Rattus.
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Hamner, S., Skoglosa, Y. and Lindholm, D.
Direct Submission
Submitted (01-07-1998) Developmental Neuroscience, Uppsala University, Box 587, BMC, Uppsala 751 23, Sweden
Location/Qualifiers
                                                181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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  Length
                         Indels
Score 567.8; DB 5;
Pred. No. 2.1e-117;
0; Mismatches 7;
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/db_xref="taxon:10116"
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/dev_stage="postnatal"
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Rattus norvegicus Bcl-w
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97.4%;
98.8%;
Query Match 97.4
Best Local Similarity 98.8
Matches 572; Conservative
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AMRAAGDEFETRFRTFSDLAAQLHYTPGSAQORFTQVSDELFCGGPNWGRLVAFFVF
AAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTYGVALGALUTYGAFFASK"
156 c 211 g 111 t
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Gibson,L., Holmgreen,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and
                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 582)

Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S. Obclew, a novel member of the bcl-2 family, promotes cell survival 0ncogene 13 (4), 665-675 (1996)
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Eliza Hall Institute of Medical Research, PO Royal Melbourne
Hospital, Parkville, Victoria 3050, Australia
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99.0%; Score 577.2; DB 10; Length 582;
Best Local Similarity 99.5%; Pred. No. 1.6e-119;
Matches 579; Conservative 0; Mismatches 3; Indels 0:
                            HSU59747 582 bp mRNA
Human Bcl-w (bcl-w) mRNA, complete cds.
U59747
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                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAB09055.1"
/db_xref="GI:1572493"
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualiflers
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/product="Bcl-w"
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1. .582
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Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayasi,Y.,
Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N.
Prediction of the coding sequences of unidentified human genes. VI.
The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain
DNA Res. 3 (5), 321-329 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (sites)
Nagase,T., Seki,N., Ishikawa,K. and Nomura,N.
Prediction of the coding sequences of unidentified human genes.VI.
The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from human cell line KG-1 and brain Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-AUG-1996) to the DDBJ/EMBL/GenBank databases. Nobun Nomura, Kazusa DNA Research Institute, Gene Structure 1; 1532-3 Yana, Kisarazu, Chiba 292, Japan (E-mail:cdnainfo@kazusa.or.jp, URL.http://www.kazusa.or.jp, Tel:0438-52-3930, Fax:0438-52-3931)
                                                                      480
421 agtgggggctgggggggggttcacagctctatacggggacgggggccctggaggaggcgcgg 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens male brain myloblast cell_line:KG-1 cDNA to mRNA, clone_lib:pSPORT 1 clone:HA6752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 3542)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUL-1997
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                                                                                                                                                                                                   DB7461 3542 bp mRNA PRI Human mRNA for KIAA0271 gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="BAA19666.1"
/db_xref="G1:1944418"
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="myloblast"
/clone="HA6752"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="pSPORT 1"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
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177. .758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_line="KG-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="KIAA0271"
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July 3, 2000, 20:45:19; Search time 888.39 Seconds (without alignments)
-638.388 Million cell updates/sec
                                                                                                                                                                                                                                                         583
1 atggcgaccccagcctcggc......cttttttgctagcaagtgaa 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1765538
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                           882769 seqs, -486395729 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                    IDENTITY_NUC Gapox 1.0
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
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                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
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45: gb_htg7:*
47: em_htg2:*
48: em_htg3:*
49: em_htg3:*
50: gb_p13:*
51: gb_pt3:*
52: gb_htg8:*
53: gb_htg9:*
54: gb_htg10:*
55: gb_htg11:*
56: gb_htg11:*
56: gb_htg11:*
56: gb_htg11:*
57: gb_htg11:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|           | ion                   | U59747 Human Bcl-w | D87461 Human mRNA |          |          | AR020779 Sequence | U59746 Mus musculu | Mus mu       | 829 Human | X82462 X.laevis Rl | U10579 Rattus norv | U72350 Rattus norv | X82537 R.norvegicu | U34963 Rattus norv | - Toq  |          | AJUULZUS SUS SCroi | .musculus | Mus      | L35049 MUS musculu | 0012/0 Mus musculu | APOSA0220 EUNELJOCE | a.     | H. sapiens | 9 Rattus no | Rattus | U92434 Bos taurus | L14680 Rattus norv | Gallus | 2 Sequenc | Φ      | AR052621 Sequence | anbac     | TOBO38 Compace 1 | ocquence | 18 HOMO SA |            | קפט טוווטה | 2010 | ARUZIIOU SEQUENCE<br>M14745 Unman hol-2 | Monda bel | Mouse oct | Mus muscul | Snus     | 500 |
|-----------|-----------------------|--------------------|-------------------|----------|----------|-------------------|--------------------|--------------|-----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|----------|--------------------|-----------|----------|--------------------|--------------------|---------------------|--------|------------|-------------|--------|-------------------|--------------------|--------|-----------|--------|-------------------|-----------|------------------|----------|------------|------------|------------|------|---|-----------|-----------|------------|----------|-----|
| SUMMARIES | Ι                     | HSU59747           | D87461            | AR020780 | AF096291 | AR020779          | MMU59746           | AF030769     | CNS0000B  | XLR1               | RNU10579           | RNU72350           | RNCBLXLS           | RNU34963           | S76513 | AF216205 | 557001203          | MMBCLAL   | MMOTOTOT | MUSBCLX            | AE060226           | AF 000220           | T52011 | HSBCLXI.   | RNU72349    |        | BTU92434          | RATBCL2A           |        | AR052622  | A76121 | AR052621          | ARU34 UUB | TOROGR           | 00000    | AC016318   | UC 1957M17 |            |      | HIMPETION                               | nombcusc. | MUSBCLZI  | MMOSIZII   | MM010102 | -   |
|           | DB                    | :                  | 6                 |          |          | വ                 | -                  | <del>-</del> |           | 4                  | -                  | Т                  | 12                 | 12                 | 12     | m c      | າ ເ                | ٦.        | ٠,       |                    | ٦-                 | 1 10                | יש ר   | _          |             | -      |                   |                    | -      | n ı       | ı D    | nι                | n c       | א ע              | , -      | 2 5        | 7 6        | 0 <        | * 1  | n a                                     | ۷ .       | 7.5       | 1 5        | 7 6      | า   |
|           | Query<br>Match Length | 582                | 3542              | 579      | 582      | 579               | 582                |              | 196287    | 749                | 764                | 1742               | 2232               | 726                | 726    | 720      | 70/                | 3 0       | 707      | 7.7                | 5771               | 900                 | 926    | 926        | 1748        | 708    | 687               | 1179               | 1184   | 717       | 765    | 5086              | 0000      | 5105             | 723      | 74673      | 151020     | 670101     | 1001 | 6030                                    | 2 5       | \$167     | ה<br>ה     | 1946     | •   |
| ф         | Query<br>Match        | 9 .                | 98.6              | 7        | 90.5     | ó.                | ė.                 | ď            |           |                    | •                  |                    |                    | ٠                  | ٠      | 23.3     | ٠                  |           |          |                    | 0.77               |                     | 22.5   |            |             |        |                   |                    |        | 21.2      |        | 21.2              | ٠         | 21.7             |          | 71.1       |            | ; ,        |      | 200                                     |           | 7.0       | ;          | 20.0     |     |
|           | ore                   | 77.                | 575               | 567.8    | 27.      | 22                |                    | 22.          | 23.       | 38.                |                    |                    | 14                 | 38                 | 8 8    |          | 500                |           | 2 2      |                    |                    | 13.0                | 131    | 131        | 129.8       | 128.6  | 128.2             | 127                | 127    | ٠         | 23     | 123.4             |           | 123.4            | , ,      |            |            |            |      | 121.8                                   |           |           |            | 120.2    |     |
|           | Result<br>No.         | -                  | 7                 | m        | 4        | ß                 | 9                  | 7            | 80        | o                  | 10                 | 11                 | 12                 | 13                 | 14     | 15       | 9 1                | 77        | 7 7      | א כי               | 202                | 22                  | 23     | 24         | 25          | 26     | 27                | 28                 | 29     | 30        |        | 3.5               |           | ე ი<br>ტ ი       |          |            | י רי       |            | 0 4  | 4 4                                     | T (       | 7 7       | 7 4        | 4 4      | 7   |

ALIGNMENTS

Oy 451 tacgg 455 ||||||| |Db 2062 TACGG 2066

Search completed: July 4, 2000, 01:24:21 Job time: 14809 sec

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2062 TACGG 2066
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                                                                                  1942 GTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG 2001
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                                                  271 cccaactggggccgccttgtagcctctttctctttggggctgcactgtgtgctgaaggt
                                                                                                                     gtcaacaaggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctg
                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application PC/TUS9305651
GENERAL INFORMATION:
TITLE OF INVENTION: A Gene Which Prevents Programmed Cell Death
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.2%; Score 123.4; DB 6; Length 5086; 58.6%; Pred. No. 8.2e-23; tive 0; Mismatches 151; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05651
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTER STICS:
LENGTH: 5086 base pairs
TYPE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: /product= "Bcl-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 58.6
Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 1459..2178
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PCT-US93-05651-4
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APPLICANT: Wickstrom, Eric and Rife, Jason P. TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                    ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT/US93/06251
                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                          Sequence 2, Application PC/TUS9306251 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 856
                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-2
                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 5086 base pairs
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 214; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                11530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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PCT-US93-06251-2
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1702 GCGGGCCTGCGCTCAGCCCGGTGCCACCTGTGCTCCACCTGGCCCTCCGCCAAGCCGGC 1761
2002 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG 2061
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                                                                                                                                                                                                                                                                                                      APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 21.2%; Score 123.4; DB 5; Length 5 Best Local Similarity 58.6%; Pred. No. 8.2e-23; Matches 214; Conservative 0; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/080,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 05-JUN 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGNY INCRMATION:
NAME: FORTHORY, ANGREW D.
REGISTRATION NUMBER: 33,5-070-55 CONT
TELEPONMUNICATION INFORMATION:
TELEPHONE: (408) 43,5-2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             ; Sequence 19, Application US/09080285
; Patent No. 6040181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
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                                                                                                     2062 TACGG 2066
                                                     451 tacgg 455
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                                                                                                                                                                                                     US-09-080-285-19
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                          GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO ORIGINAL SOURCE: INDIVIDUAL ISOLATE: human bc1-2 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/365,486A FILING DATE: 23-DEC-1994 CLASSIFICATION: 514
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NAME: Sholtz, Charles K.
REGISTARION UNDER: 38.615
REFERENCE/DOOKET NUMBER: 8255-
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 5086 base pairs
TYPE: nucleic acid
STRANDEDNES; double
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; LOCATION: 1459..2178
US-08-365-486A-14
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RESULT 12
US-08-365-486A-14
: Sequence 14, Application US/08365486A
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Patent No. 581066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arilington
                                                                           RESULT 10
5459251-1
;PAREDI NO. 5459251
; AAPLICANT: TSUJIMOLO, YOSHIĞE;CTOCE, CATIO A.
TITLE OF INVENTION: DNA MOLECULES HAVING HUMAN BCL-2 GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 123.4; DB 7; Length
Pred. No. 8e-23;
0; Mismatches 151; Indels
                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/228,704
FILING DATE: 18-APR-1994
PRION APPLICATION DATA:
APPLICATION NUMBER: 994,941
FILING DATE: 23-DEC-1992
APPLICATION NUMBER: 663,010
FILING DATE: 19-MAR-1991
APPLICATION NUMBER: 883,687
FILING DATE: 09-JUL-1986
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58.6%;
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Best Local Similarity
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451 tacgg 455
                             604 TACGG 608
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US-08-465-485A-19
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                                                                                                                                                           SEQUENCES:
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2002 AACCGGCACCTGCACCAGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG 2061
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                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: US-JUN-1995
CLASSIFICATION: 514
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                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INCRMATION:
NAME: FORTHORY, ANGREW D.
REGISTRATION NUMBER: 34,600
REGISTRATION NUMBER: 34,600
REGISTRATION NUMBER: 34,600
RECEMENCE/DOCKET NUMBER: 3335-070-55 CONT
TELEPRIONE: (408) 436-2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 8.2e-23
0; Mismatches 15
                                                                                                            PC-DOS/MS-DOS
                                                                                       IBM PC compatible
                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (408) 436-2075 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5086 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 58.6
Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                            OPERATING SYSTEM:
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U.S.A.
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US-08-465-485A-19
                                                                                       COMPUTER:
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Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
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                                                                                                                                       NAME: Forthey, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMUNICATION INFORMATION:
TELEPRONE: (408) 436-2070
TELEPRONE: (408) 436-2075
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                          APPLICATION NUMBER: US 07/840,716 FILING DATE: 21-FEB-1992 PRIOR APPLICATION DATA:
                                                                                         APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
US 08/124,256
                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
               FILING DATE: 20-SEP-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                           LENGTH: 717 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 214; Conservative
 APPLICATION NUMBER:
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US-08-465-485A-20
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Best Local Similarity
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US-09-080-285-20
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                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fortney, Andrew D. REGISTRATION NUMBER: 34,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAN: (408) 436-2075
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
LENGTH: 717 base pairs
TYPE: nucleic acid
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                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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               U.S.A.
Virginia
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; LOCATION: 1..7
US-09-080-285-20
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                           22202
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                 COUNTRY:
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                                     0; Gaps
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22.5%; Score 131; DB 3; Length 926; 56.3%; Pred. No. 6e-25;
                                   0; Mismatches 190; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DS/MS-DOS, ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07089
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CONCURRENTLY FILED
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States of America ZIP: 77210
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APPLICANT:
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REGISTRATION NUMBER: 32,165
RELECOMMULCATION INFORMATION:
TELEPHONE: 512-320-7200
INFORMATION FOR SEQ 1D NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/081
FILING DATE: 22 JUNE 1993
ATTORNEY/AGENT INFORMATION:
                                 Matches 245; Conservative
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STREET: P.O. Box 4433
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                Local Similarity
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STATE: TX
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TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                                                                                                       Score 131; DB 6; Length 92
Pred. No. 6e-25;
0; Mismatches 190; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 20, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                       22.5%;
ilarity 56.3%;
Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                135..836
                                       linear
                                                                                                                                                                                                           Similarity
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                                                                                          ; NAME/KEY:
; LOCATION:
PCT-US94-07089-6
                                       TOPOLOGY:
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421 agtggggggctggggggggttcacagctctatacgggggacgggggccctggagggggcgcgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Arnold, White & Durkee
321 No. 5646008th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Thompson, Craig B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: No. 5646008thrup, Thomas E.
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-744-0090
                                                                                                                                                                                                                                           RESULT 5
US-00-081-448-5
; Sequence 5, Application US/08081448
; Patent No. 5646008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMPONE: 312-74* CTELEPHONE: 312-75-4489
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 926 base pairs TYPE: nucleic acid TYPE: nucleic acid TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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LOCATION: 135..836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 321 No CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                            278 ggggccgcttgtagccttctttttggggctgcactgtgtgctgagagtgtcaaca 337
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,670A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Thompson, Craig B. B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CIASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 22-UNN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: 37,642
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 6, Application US/08470670A
; Patent No. 5834309
; Patent No. 5834309 5710045
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TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
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ZIP: 77210
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, LOCATION:
US-08-470-670A-6
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                                                                                                                                                                                                                                                                                                Length 579;
                                                                                                                                                                                                                                                                                                                      35; Indels
            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARLENLIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 89.7%; Score 523; DB 2;
Best Local Similarity 94.0%; Pred. No. 1e-124;
Matches 544; Conservative 0; Mismatches 35
                                                                                                                        1483.0140001
                                                             FILING DATE: February 11, 1997
CLASSIFICATION: 435
                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2500
TELEFAX: 202-371-2540
IBM PC compatible
                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 579 base pairs TYPE: nucleic acid STRANDEDNESS: both
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MOLECULE TYPE: CDNA
US-08-798-897-1
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Sequence 1, Application US/08978523 Patent No. 5883229

US-08-978-523-1

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               APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDER ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                       ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
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                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
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NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 14:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
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Matches 544; Conservative
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US-08-978-523-1
                                                                                                                                                CLTY: Washington STATE: Pr
GENERAL INFORMATION:
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: herewith
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION UNDRER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
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; Sequence 2, Application US/08978523
; Patent No. 5883229
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202-371-2540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
                                                                                                                                                                                                                                                       241 CAGGICICCGAIGAACITITICAAGGGGGCCCCAACIGGGGCCGCCTIGIAGCCTITTIT 300
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                            1 ATGGCGACCCCCAGCCTCGGCCCCAGACACGCGCTCTGGTGGAAGACTTTGTAGGTTAT 60
                                                                                                                                                                                                  1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
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0
                                                                                                                                         Length 579;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: ... STERNE, KESSLER, GOLDSTEIN & FOX P. CIIY: Washington STATE: DC
                                                                                                                                          Score 567.8; DB 3;
Pred. No. 4.2e-136;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08798897 Patent No. 5789201
                                                                                                                                             97.48;
98.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
             SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                        Matches 572; Conservative
INFORMATION FOR SEQ ID NO:
                                                                                 , MOLECULE TYPE: CDNA
US-08-978-523-2
                                                                                                                                                           Local Similarity
                                                                      TOPOLOGY: both
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20005
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US-08-798-897-1
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Best Local S
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July 3, 2000, 21:17:32 ; Search time 57.05 Seconds (without alignments) 1328.331 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 20, Appl
Sequence 20, Appli
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Sequence 16, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 3, Appli
Patent No. 5459251
Patent No. 5506344
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Patent No. 5506344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Appl
Sequence 19, Appl
Sequence 4, Appli
Sequence 2, Appli
Patent No. 5506344
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                               1 atggcgaccccagcctcggc......ctttttgctagcaagtgaa 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2
Sequence 2
Patent No.
                                                                                                                                                                                                                                                                                                                              Issued_Patents_Nh:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/FOTUS_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/PoTUS_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/PoTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-798-897-1
US-08-978-523-1
US-08-08-448-5
US-08-470-670A-6
US-08-46-47089-6
US-08-46-4858-20
US-09-080-2855-20
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US-08-365-486A-14
US-09-080-285-19
PCT-US93-05651-4
PCT-US93-06251-2
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US-08-405-702A-11
US-08-365-486A-16
US-08-465-485A-22
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PCT-US94-07089-1
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US-08-978-523-2
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                                                                                                                                                                                                         230463 seqs, 64992525 residues
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                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Listing first 45 summaries
                                              OM nucleic - nucleic search, using sw model
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                                                                                                                                                                      IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                      US-09-155-327B-6
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Maximum DB seq length: 1000000
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Match Length
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926
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                                                                                                                                 Perfect score:
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567.8
523
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131
131
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120.2
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                                            Sequence 8, Apsequence 1, Apsequence 1, Apsequence 1, Apsequence 1, Apsequence 20, Assequence 20, Assequence 14, Assequence 1, Apsequence 1, Apsequence 1, Apsequence 1, Apsequence 1, Apsequence 1, Apsequence 75, A
               Sequence 8,
Sequence 8,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: COUNTRY: USA
ZUDNUTRY: USA
ZUDNUTRY: 120005
COMPUTER PADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SPETWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.4%; Score 567.8; DB 2;
98.8%; Pred. No. 4.2e-136;
ive 0; Mismatches 7;
         US-08-470-6708-9
US-08-170-6708-8
US-08-112-208C-1
US-08-112-208C-1
US-08-248-819A-1
US-08-856-531-1
US-08-856-531-1
US-08-856-531-1
US-08-856-531-1
US-08-471-058-20
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US-09-915-246-1
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US-09-180-23-46-1
US-08-180-23-46-1
US-08-180-23-46-1
US-08-180-23-46-1
US-08-180-23-46-1
US-08-180-23-46-1
US-08-186-250-3
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08798897; Patent No. 5789201; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEO ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
737
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628
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628
7218
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688
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MOLECULE TYPE:
US-08-798-897-2
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US-08-798-897-2
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Gaps

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Indels

1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60 

Best\_Local Similarity 98.8 Matches 572; Conservative

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                                                                                                                                                                                                                                                                                                                           314 cactgigigicigagagigicaacaaggagatggaaccactggigggacaagigcaggagi 373
                                                                                                                                                                                                                                                                          168 CCAGCCAGCACCTGACGCCCTTCACCGCGGGGACGCTTTGCCACGGTGGTGGAGG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                    248 TCATGTGTGTGAGGAGGGTCAACCGGGAGATGTCGCCCTGGTGGACAACATCGCCCTGT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single read.
Genexpress_lbrary_idt: C; Genexpress_sequence_idt: y3c-25b06
Genexpress_lbrary_idt: C; Genexpress_sequence_idt: y3c-25b06
Insert Length: 1145 Std Error: 0.00
Seq primer: (-21)M13_universal
High quality sequence stop: 339.
Location/Qualifiers
                                                                                                                                                                                 134 ccatgogggcagctggagatgagttcgagaccogcttccggcgcaccttctctgatctgg 193
                                                                                                                                                                                                                                                         194 eggeteagetgeatgtgacceaggeteageceageaacgetteacceaggtetecgacg 253
                                                                                                                                                                                                                   Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genethon Centre de recherche sur le Genome Humain
1,rue de 1'Internationale, BP60 91002 EVRY Cedex, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Sep 21, 1992 this sequence version replaced gi:276079
                                                                                                                                               ö
                                                                                                             DB 46; Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995) 95277534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="normalized infant brain cDNA"
                                                                                                         Score 111.2; DB 46; Length
Pred. No. 2.7e-16;
0; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Female"
/tissue_type="total brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="c-25b06"
                                                                                                             19.18;
60.78;
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                                                                                                                                               Matches 182; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 33169472800
Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                         91
                                                                                                             Query Match
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MEDLINE
COMMENT
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                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
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SOURCE

LOCUS

Search completed: July 4, 2000, 01:06:08 Job time: 16527 sec

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/note="Organ: brain; Vector: lafmid BA, Site_1: HindIII; Site_2: NotI; sex=Female; dev_stage=3 months old; Site_2: NotI; sex=Female; dev_stage=3 months old; sloal*te=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Soares, Psychiatry Dept. Columbia University, USA. Normalization_method: Bento Soares, P.N.A.S in press a 69 c 94 g 67 t 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GGGGTAAACTGGGGTCGCATTGTGGCCCTTTTTCTCCTTCGGCGGGCACTGTNCGTGGAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 gtgaccccaggctcagcccagcacgcttcacccaggtctccgacgaacttttcaaggg 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggccccaactggggccgccttgtagccttctttctcttttggggctgcactgtgtgctgag 327
                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
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18.8%; Score 109.6; DB 21; Length
Best Local Similarity 61.2%; Pred. No. 5.5e-16;
Matches 175; Conservative 0; Mismatches 111; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: mob.REGA+ET High quality sequence stop: 383.

Location/Qualifiers
                              Gaps
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 437)
Halliler, L., Clark, M., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Ruchada, T., Le, M., Lennon, C., Marra, M.
Parsons, J., Rikin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The MashU-Merck EST Project
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:785898.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fel: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                              385 tacctggagacgcggctggtcgactggatccacagcagtgggggctggg 433
                                                                                                                181 TACCTGAACCGCATCTGCACACCTGGATCCAGGATAACGGAGGCTGGG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.6%; Score 114.2; DB 25; Length 62.9%; Pred. No. 5.4e-17; Live 0; Mismatches 113; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="IMAGE:298187"
/clone_11b="Soares_fetal_lung_NDHL19w"
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/db_xref="GDB:1243109"
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Best Local Similarity 62.99
Matches 193; Conservative
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                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                               RESULT 13
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128 accaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcaccttctctg 187

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Unpublished (1997)
On Apr 7, 1998 this sequence version replaced gi:3035272.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement. Ash Alizadeh, John Byrd, M.D., Mike Grever,
Tissue Procurement. Ash Alizadeh, John Byrd, M.D., Mike Grever,
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1999 30-MAR-1999 1492c06.x1 NCI_CGAP_CILI Homo sapiens cDNA clone IMAGE:2116234 3' similar to gb:MI3995 PROTEIN BCL-2-BETA (HUNAN);contains TARI.t2 MER22 repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 471)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                             76 ACCTGACATCCCAGATCACCCCAGGACAGATATCAGAGCTTTGAACAGGTAG 135
                                                                                                                                                                                                                                    136 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGGCTTTTTCTCCCTTCG 195
                                                                                                                                                                                                                                                                                                        308 gggctgcactgtgtgtggtgagagtgtcaacaaggagatggaaccactggtgggacaagtgc 367
                                                                                                                                                                                                                                                                                                                                                              196 GCGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG 255
                                                                                                                                                                                                                                                                                                                                                                                                                     368 aggagtggatggtggcctacctggagacgcggctggtcgac-tggatccacagcagtggg 426
                                                                                  188 atctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacccaggtct 247
                                                                                                                                                                                                 248 ccgacgaacttttcaagggggccccaactggggccgccttgtagccttcttctttttg 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAAGCCTTGGATCCAGGAGGGC 315
16 AGCAAGCGCTGAGGGAGGCAGGCGACGAGGTTTGAACTGCGGGTACCGGCGGCGCATTCAGTG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/tissue_type="B-cell, chronic lymphotic leukemia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      www-bio.llnl.gov/bbrp/image/image.html
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High quality sequence stop: 445.
Location/Qualifiers
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Unpublished (1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .471
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/do.xere="cason:10090"
/clone="11b-"NIH_BMAP_M_S3.1"
/dov.stage="27-32 days"
/dov.stage="27-32 days"
/dov.stage="27-32 days"
/dov.stage="27-32 days"
/dov.stage="27-32 days"
/dov.stage="DH10B (Life Technologies)"
/note="vector: pT773D-pac (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: ECO RI; The
NIH_BMAP_M_S3.1 library is a subtracted library of a
series, ultimately derived from a mixture of individually
tagged normalized libraries from ten regions of the mouse
brain (cerebellum, brain stems, olfactory bulbs,
hypothalamus, cortex, amygdala, basal ganglia, pineal
gland, striatum, hipoccampus) after a series of
subtractions to reduce the representation of cDNAs from
which ESTs had already been generated. The following
serially subtracted libraries were generated in this
process: NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1) was constructed
as follows: PCRamplified CDNA inserts from NIH_BMAP_M_S2
clones from which 3' ESTs had been derived was used as a
driver in a hybridization with the NIH_BMAP_M_S2 library
in the form of single-stranded circles (subtracted library) was purified
by hydroxyapatite column chromatography, converted to
by hydroxyapatite column chromatography, converted to
by harder is a process of the column chromatography to the plant
determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. Seq primer: M13 Forward POLYA-No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bacteria (Liferechnologies) to generate the NIH,BMAP,M.S3.1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 cageceageaacgetteaceeaggtetecgaegaactttteaagggggeeceaaetggg 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              281 gccgccttgtagccttctttctctttggggctgcactgtgtgctgagagtgtcaacaagg 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 agatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgcgggc 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 gggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagttcg 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 1.5e-17;
0; Mismatches 134; Indels 0;
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TAG_TISSUE=hippocampus
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                                                                                                                                                                                                                       /strain="C57BL/6J"
/db_xref="taxon:10090"
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Best Local Similarity 59.5%;
Matches 197; Conservative (
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 catgtgacccoaggctcagcccagcaacgcttcacccaggtctccgacgaacttttcaa 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 gotggagatgagttcgagacccgcttccggcgcaccttctctgatctggcggctcagctg 204
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                                  01-MAY-1998
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 515)
                                  AA939725 515 bp mRNA EST 01-MAY-199 vz92a11.rl Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1344668 5' similar to gb:L31532_rna1 Mouse bcl-2 gene encoding mbcl-2-beta (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1996)
On Jan 19, 1998 this sequence version replaced gi:2285479.
Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1880
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="TyAGE:1344668"
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 304.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
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                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                 house mouse.
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Best Local S
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RESULT 12
AA939725/c
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                                                           DEFINITION
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JOURNAL
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Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).
EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and
Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
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This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                101 gggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagttcg 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cagcccagcaacgcttcacccaggtctccgacgaactttttcaagggggccccaactggg 280
                                                                                                                                                                                                                                                                                                                                                                                                               agacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccaggct 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 gccgccttgtagccttctttttggggctgcactgtgctgagagtgtcaacaagg 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341 agatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgcggc 400
                                                                                                                                                                                                                                                                                                                                                           383 GGGAGGTAATCCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGGCTGGCGATGAGTTTG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                          323 AACTGCGGTACCGGAGGGTTCAGTGATCTAACATCCCAGCTTCATATAACCCCAGGGA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 CAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTTCGGGGATGGGGGTAAACTGGG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL134785 584 bp mRNA EST 29-DEC-1999
DKF2D547K2090_r1 547 (synonym: hfbrl) Homo sapiens cDNA clone
AL134785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heldelberg/Germany) within the CDNA sequencing consortium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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On Jul 7, 1999 this sequence version replaced gi:5866255.
Contact: Poustka A.J.
Contact: Poustka A.J.
Max-Planck-Institute for Molecular Genetics
Max-Planck-Institute for Molecular Genetics
Thestrasse 73, 14195 Berlin, Germany
Tel: +49-30-84131623
Fax: +49-30-8413128
Email: poustka@mping-berlin-dahlem.mpg.de
                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                     Score 125.8; DB 51; Length 404;
Pred. No. 1.1e-19;
0; Mismatches 127; Indels 0;
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                                                                                                                        92
                                             TAG_LIB=UI-R-Y0
TAG_TISSUE-Eye
TAG_SEQ=CATTG"
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61.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mEST@mail.nih.gov Oligious and the shown in beginning of sequence Oligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. CDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP CDNA clones will be made available by the means that is soon to be determined. When NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 tcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccag 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 ccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157
                                                                                                                                                                                                                                                                                                                                                                                                                                       gotcagoccagoacgottcacccaggtctccgacgaacttttcaagggggccccaact 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   383 GCACAGCATATCANAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGGATGGGGTAAACT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggggccgccttgtagccttctttctctttggggctgcactgtgtgctgagagtgtcaaca 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        443 GGGTCGCATTGTGGCCTTTTTCTCCTTCGGCGGGCACTGTGCGTGGAAAGCGTAGACA 502
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                /note="Vector: pAMP1; Site_1: Not1; Site_2: Sal1"
145 c 173 g 116 t 6 others
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Jul 7, 1999 this sequence version replaced gi:5866278.
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                                                                                                                                                                                                                                                                                                            Score 119.4; DB 79; Length 584;
Pred. No. 3.7e-18;
0; Mismatches 127; Indels 0;
                                                                                  /clone="DKFZp547K2090"
/clone_lib="547 (synonym: hfbr1)"
/tssue_type="brain"
/dev_stage="fetal"
/lab_host="Xl-2blue"
                                      /organism="Homo sapiens"
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                                                                /db_xref="taxon:9606
Location/Qualifiers
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60.2%;
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Best Local Similarity 60.29
Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 301 443 1706
Fax: 301 443 9890
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
7e1: (206) 616-3887
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
clones are derived from the human BAC library RPCI-11. For BAC
library availablility, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 638 row: M column: 4
Seq primer: 8766
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 455)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HS_5062_A2_G02_SP6E_RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=638 Col=4 Row=M, genomic survey sequence.
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111 c 142 g 117 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                      492 ggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactggggccctggt 551
                                                                                                                                                                                                                              321 GGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGGT 380
                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-1999
Score 148.8; DB 109; Length 549;
Pred. No. 5.5e-25;
0; Mismatches 2; Indels 0;
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Mahairas GG, Wallace JC, Hood L
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/clone="Plate=638 Col=4 Row=M"
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Location/Qualifiers
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  25.5%;
98.7%;
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92.8%;
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Best Local Similarity
                          Similarity
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                                             Matches 150;
    Query Match
                            Best Local
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0; Gaps

11; Indels

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Matches 141; Conservative

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/organism="Spratus norvegicus" / Strain="Spratus norvegicus" / Strain="Spratus norvegicus" / Strain="Spratus norvegicus" / Strain="Spratus norvegicus" / Clone_11D="UI.R-Y0-acg-9-07-0-UI" / Clone_11D="UI.R-Y0-acg-9-07-0-UI" / Clone_11D="UI.R-Y0-acg-9-07-0-UI" / Iab_host="Duling Life Technologies)" / Alab_host="Duling Life Technologies)" / Alab_host="Duling Life Technologies)" / Alab_host="Strein" in Strein of Isters is a subtracted library derived from an individually-tagged normalized whole-eye (mins the lens) library. The driver for the subtraction consisted of a pool of all previous libraris (UI-R-AO, UI-R-A), UI-R-EO, UI-R-EI, UI-R-CO, and UI-R-CI). The tag is a string of UI-R-EI, UI-R-CO, and UI-R-CI). The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dr track which allows identification of the library of origin of a clone within the mixture. The subtracted library of origin of a clone within the mixture. The subtracted library of origin of a clone within the mixture as under eye library in the form of single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-Y0 library. This procedure has been previously described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: msoares@blue.weeg.ulowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
Seq primer: M13 Forward
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
224 GGGGGAGTTCACAGCTCTATACGGTGACAGCGCCCTGGAGGATGCGCGGGGTCTCCGGGGA 283
                                                                                          492 ggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactgggggccctggt 551
                                                                                                                                                         284 GGGGAACTGGGCATCAGTGAGGACAGTGCTGACNGTGGCCGTGGCACTTGGGGCCCTTGT 343
                                                                                                                                                                                                                                                                                                                                                                                                                                           AI716839 404 bp mRNA EST 10-JUN-1999 UI-R-YO-acg-g-07-0-UI.s1 UI-R-YO Rattus norvegicus CDNA clone UI-R-YO-acg-g-07-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On May 18, 1998 this sequence version replaced gi:3136946.
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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                                                                                                                                                                                                                  Genome Res. 6 (9), 791-806 (1996)
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Rattus norvegicus
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Gaps

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High Throughput Sequencing Center
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Seq Primer: 17
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 549)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                              /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
130 c 237 g 133 t 1
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126 c 190 g 118 t 10 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ665088 549 bp DNA GSS 23-JUN-1999
HS_5340_B1_A06_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=916 Col=11 Row=B, genomic survey sequence.
AQ665088
                                                                                                                                                                                                                                                                                                                                                                                     Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
                                                                                                                                                                                                                                                                                                    432 ggcggagttcacagctctatacggggacggggccctggaggaggcgcggcgtctgcggga 491
                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                                                                       26.1%; Score 152; DB 108; Length 628; 100.0%; Pred. No. 1e-25; tive 0; Mismatches 0; Indels 0
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/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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Location/Qualifiers
      /clone_lib="RPCI-11"
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                         /sex="Male"
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used for subtraction consisted of a pool of 5,000 clones from the NIH_BMAP_M_S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries.

TAG_LIB=NIH_BMAP_M_S2
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RPCI-11-352L5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-352L5,
genomic survey sequence.
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Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bcpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building Unpublished (1997) On Feb 19, 1999 this sequence version replaced gi:4145213. Other_GSSs: RPCI-11-352L5.TJ
                                                                                                                                                                                                                                                                                                                                           250 gacgaactttttcaagggggccccaactggggccgccttgtagccttcttttctcttttggg 309
                                                                                                                                                                                                                                                                                                                                                                   310 gctgcactgtgtgtgtgagagtgtcaacaaggagatggaaccactggtgggacaagtgcag 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 gagtggatggtggcctacctggagacgcggctggtcgactggatccacagcagtggggc 429
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
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                                                                                                                                                                                                                                                   DB 64; Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics
The Institute for Genomic Research
7712 Medical Center Dr., Rockville, MD 20850
781: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                             17; Indels
                                                                                                                                                                                                                                                   26.9%; Score 156.8; DB 6.90.8%; Pred. No. 7.1e-27;
                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                 TAG_TISSUE=corpus-striatum
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/db_xref="GDB:7635052"
/db_xref="taxon:9606"
/clone="RPCI-11-352L5"
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Schutz, K., de la Bastide, M., Huang, E.N., Nascimento, L., Preston, R., Shah, R., Swaby, I., Shekher, M., Spiegel, L., Vil, M.D. and McCombie, W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Vector: Lambda Zap I; Site_1: XbaI; This library was supplied by Holly Cline (Cold Spring Harbor Labs). cDNA synthesis with oligo dT Xba I (Xba I cloning site). RNA: stage 50.56 tadpoles, total brain tissue, GTC
                                                                                                                                                                                                                                                                                                                                                 амізунова 416 bp mRNA EST 05-NOV-1999
za50h02.x1 Xenopus EST library Xenopus laevis cDNA clone za50h02
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                             121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
        61 aagetgaaggcagaagggttatgtetgtggagetggeeeegggggagggeeeageagetgae 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expressed sequence tags from Xenopus Expressed sequence tags from Xenopus Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3189433. Contact: W. Richard McComble
Litta Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 884
Fax: 516 367 884
Email: mccomble@cshl.org
Plate: za50 row: h column: 02
Seq primer: M13 universal forward primer
High quality sequence stop: 416.
                                                                                                           214 AAGCTGAGGCAGAAGGGGTATGTTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 160.6; DB 71; Length 416;
Pred. No. 9.2e-28;
                                                                                                                                                                                                                                            /clone_lib-"Xenopus EST library"
/tissue_type-"total brain tissue"
/cell_line="W22-TGA"
/dev_stage-"tadpole"
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/db_xref="taxon:8355"
/clone="za50h02"
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Email: mEST@mail.nih.gov
The Sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonsfide poly A tail. The Sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized corpus striatum library cDNA library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP CDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. Seq primer: MI3 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  house mouse.

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 431)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW048567 431 bp mRNA EST 18-SEP-1999 UI-M-BH1-alx-e-10-0-UI.S1 NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BH1-alx-e-10-0-UI 3', mRNA sequence.
356 tgggacaagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatcc 415
                                416 acagcagtgggggctgggggggttcacagctctatacgggggacgggggccctggaggagg 475
                                                                                                                                                                125 AGAGCAATGGATGCTGGAATGGATTTCTAACTCTATATGGGGATGGTGCCATAGAAGAAG 184
                                                                                                                                                                                                                         476 cgcggcgtctgcggggaagggaactgggcatcagtgaggacagtgctgacgggggccgtgg 535
                                                                                                                                                                                                                                                                                 185 CCAGGAGGCAACGTGAGGGGAATTGGGCATCACTGAAGACTGTCTTAACTGGAGCGGTAG 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Chin, Hall Health
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UI-M-BH1-alx-e-10-0-UI"
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/organism="Mus musculus"
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97044477
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AW048567.1 GI:5909096
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Fax: 301 443 9890
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79; Indels

Matches 208; Conservative

296 tetttetetttggggetgeaetgtgtgetgagagtgteaacaaggagatggaaccaetgg 355

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ctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcaccttc 183
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/db_xref="taxon:9913"
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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 10 row: G column: 24
Seq primer: ATTTAGGTGACACTATAG.
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/lab_host="DH108"
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Best Local Similarity
Matches 266; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mus.
Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
I (bases 1 to 362)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                          vo21f08.rl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:1050567 5' similar to TR:E123735 E123735 R1 MRNA. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information.
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                                                                                           19-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 gcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttataag 63
                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
On Dec 18, 1996 this sequence version replaced gi:1734345.
On Dec 18, 1996 this sequence version replaced gi:1734345.
On Dec 18, 1996 this sequence version replaced gi:1734345.
On Dec 18, 1996 this sequence version replaced gi:1734345.
Washington University School of MedicineP
Washington University School of MedicineP
Washington University School of MedicineP
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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/db_xref="taxon:10090"
/clone="InAGE:1050567"
/clone_llb="Bastead mouse myotubes MPLRB5"
/cell_line="C2C12"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 334. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .362
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                 AA596919.1 GI:2412354
 531 AGTGGGGGCT 540
                                                                                                                                                                                                                      house mouse.
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                                                                                                                                                                  AA596919
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                                                                        AA596919
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Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 433)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                              184 tctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
On Dec 20, 1995 this sequence version replaced gi:1133576.
Contact: Smith TPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20104 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                304 tttggggctgcactgtgtgtgctgagagtgtcaacaag 339
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| COMMENT On May 18, 1998 this sequence version replaced gi:3137956. | Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:1009678 Seq primer: custom primer used High quality sequence stop: 465. FEATURES Location/Qualifiers | source 1. :50 pure musculus"  /organism="Mus musculus"  /strain="657BL"  /db.xref="taxon:10090"  /clone="InAGE:1300906"  /clone="InAGE:1300906"  /dev_stage="adult"  /dev_stage="adult"  /dev_stage="adult"  /dev_stage="bhlost"  /dev_stage="bh | and cloned into distinct Drail sites of the PMEISS-FL3 and cloned into distinct Drail sites of the PMEISS-FL3 vector (5' site CACTGTGG, 3' site CACCATGTG). XhoI should be used to isolate the CDNA insert. Size selection was performed to exclude fragments (1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAGGTGGG and 3' end primer CGACTGCAGCTGGAGCACA."  BASE COUNT 98 a 165 c 170 g 107 t | Quer<br>Best<br>Matc   | aagccgaggcagaagggttaggccgggggcggggcgggg |   | Oy 301 ctctttggggctgcactgtgtgctgaaagtgtcaacaagagatggaaccactggtggga 360   1   |  |
|--|---|--|---|--|---|---|--|--|
| Description  | AW258B10 um74a02.y<br>AAS96919 vo21f08.r<br>AW326901 20104 WAR<br>AW159063 za50h02.x<br>AW048567 UT-M-BH1-<br>AG532175 RPCT-11-3<br>AQ6508B HS_5340_B<br>AQ401160 HS_5062_A<br>AL716839 UT-R-Y0-a<br>AL134785 DKF2E547K<br>AW124015 UT-M-BH2.   | AAA939725 vz92all.r<br>W01420 za73d06.rl<br>AI401297 t992c06.x<br>F08773 HSC25B061 n<br>AI180733 ub91d09.r<br>AA509753 vh52c06.r<br>AR149300 Rattus no<br>AW418903 ha15d05.x<br>T29044 EST66242 Hu<br>H09844 ym05b07.rl<br>AW072826 xa42e07.x<br>AA981864 ua36907.x  | A1326919 mj39801.x A1326919 mj39801.x A1326919 mj39801.x A102074 ub01h112.r AA45824 v948803.r A132304 mj39b01.y A1322704 mj39b01.y W42014 mb16904.r1 AA015184 mh33312.r AA015181 mj41h10.r W97433 mf95f12.r1  | AL05930.2 Drosophil<br>AL053013 Drosophil<br>AL063013 Drosophil<br>AL107098 Drosophil<br>AL07098 Drosophil<br>AA049970 mj39b01.r<br>AL105055 Drosophil<br>AL105055 Drosophil<br>AL065132 Drosophil | EST 23-DEC-1999                         | is musculus cDNA clone<br>UNSE P70345 APOPTOSIS<br>mRNA seguence.   | <pre>i; Vertebrata; Mammalia; idae; Murinae; Mus. in,J., Beck,C., Wylie,T., Allan,M., Bowers,Y., c,Cardenas,M., McCann,R.,</pre>   |  |
| e Match Length DB ID   | 61.3 540 79 49.4 362 35 44.2 416 79 27.5 416 71 26.9 628 108 25.5 549 109 23.3 455 106 20.5 584 79  |  | 8.4<br>8.2<br>8.2<br>8.1<br>8.1<br>8.1<br>8.1<br>8.0<br>8.0<br>8.0<br>8.0<br>8.0<br>8.0<br>8.0<br>8.0   | 7.8 925<br>7.8 925<br>7.8 1101<br>7.8 1101<br>7.7 1446<br>7.7 1084<br>7.7 1084   | ALIGNMENTS W258810 540 bp mRNA          | um74a02.yl Sugano mouse kidney mkia Mus musculus cDI<br>IMACE:2300906 5' similar to SW:BCLW_MOUSE P70345 APC<br>REGULATOR BCL-W. [2] SW:BCLW_MOUSE ;, mRNA sequence<br>AW258810.1 GI:6631791<br>EST.<br>Muse mouse.<br>Mus musculus | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodeniia; Sciurognathi; Muridae; Murinae; Mus.  1 (bases 1 to 540) Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Onderwood, K., Steptoe,M., Theisingy,B., Allen,M., Bowers,T., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., The WashU-NCI Mouse EST Project 1999 Unpublished (1999) |  |
| No. Score  | 10<br>8<br>10<br>11   | c 12 114.6<br>c 14 1114.2<br>c 15 109.6<br>c 16 108.8<br>c 17 104.6<br>c 20 52.8<br>c 20 52.8<br>c 22 52.6<br>c 23 50.2<br>c 24 49   | 20000000000000000000000000000000000000  |  | RESULT 1<br>AW25810<br>LOCUS AW         | ITION<br>SION<br>ON<br>RDS<br>E   | ल्ल न  |  |

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Ouery Match 16.5%; Score 231; DB 1; Length 192; Best Local Similarity 27.3%; Pred. No. 4.44e-25; Matches 33; Conservative 36; Mismatches 47; Indels 5; Gaps 4;
                                                                                                                                                                                                                                                                                                                                                        50 PPQDASTKKLSECLRRIGDELDSNM--ELQRMIADVD-T-DSPREVFFRVAADMFADGNF 105
                                                                                                                                                                                                                                                                                                             MGD; MGI:99702; BAX.

R PROSITE; PS01080; BH1; 1.

R PROSITE; PS01259; BH2; 1.

R PROSITE; PS0062; BCL2_FAMILY; 1.

R POPLOSIS; Transmembrane; Alternative splicing.

R DOMAIN 98 118 BH1.

R DOMAIN 98 118 BH1.

R DOMAIN 150 165 BH2.

R TRANSMEM 172 192 POTENTIAL.

SEQUENCE 192 AA; 21394 MW; D2E0B3566579FAFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              166 G 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH HIGHEST LEVELS IN THE TESTIS AND OVARY.

-i- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK AND BAX FOR THEIR KILLING ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).

-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).

-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
                                                                                                                                                                                                                                                                                                                                                                                                                                "Expression of members of the bcl-2 gene family in the immature rat covary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xing messenger ribonucleic acid levels."; Endocrinology 136:232-241(1995).
--- FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTAGONIZING THE APOPTOSIS REPRESSOR ECL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C, ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.

-!- SUBJUTT: FORMS HOMODIRERS AND HETEROITMERS TOGETHER WITH BCL-2, E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.

-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.

-!- ALTERNATIVE PRODUCTS: A 21 KD KREBRANE PROTEIN ALPHA AND THE TWO CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
                                                                                                                                                                                                                                                        Madison D.L., Pfeiffer S.E.; "Cloning of the 3' end of rat bax-alpha and corresponding developmental down-regulation in differentiating primary, cultured
                                                                                             Han J., Sabbatini P., Perez D., Rao L., Modha D., White E.; "The ElB 19K protein blocks apoptosis by interacting with and inhibiting the p53-inducible and death-promoting Bax protein."; Genes Dev. 10:461-477(1996).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS50062; BCL2; FAMILY; 1.
PROMIP PF00452; BCL-2; 1.
Apoptosis; Transmembrane; Alternative splicing.
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                         Neurosci. Lett. 220:183-186(1996).
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EMBL, U59184; AAC5298.1; --
EMBL, U32098; AAA75200.1; --
EMBL, SC6111; AAC60700.1; --
EMBL, U49729; AAC6327.1; --
HSSP, P53563; IAF3.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 37-169 FROM N.A.
                                                                                                                                                                                                   SEQUENCE OF 75-192 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118
165
192
72
                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-SPRAGUE-DAWLEY; MEDLINE; 95129487.
                                                          SEQUENCE FROM N.A.
                                                                               MEDLINE; 96178771
                                                                                                                                                                                                                                         MEDLINE; 97147318.
                                                                                                                                                                                                                                                                                                                       oligodendrocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPLICING.
                                                                                                                                                                                                                         TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
-!- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK AND BAX FOR THEIR KILLING ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-!- SIMILARITY: CONTAINS A BCL-2 PAMILY.
                                                                                                                                                         PPQDASTKKLSECLRRIGDELDSNM--ELQRMIADVD-T-DSPREVFFRVAADMFADGNF 105
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CESSATION OF SPERM PRODUCTION.
-!- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
-!- ALTERNATIVE PRODUCTS: A 21 KD MEMBRANE PROTEIN ALPHA AND THE TWO
CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
                                                                                                                                                                                      33 PGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGP- 91
                                                                                                                           ς;
Έ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                              Length 192;
                                                                                                                         36; Mismatches 47; Indels
L -> M (IN REF. 2).
C -> Y (IN REF. 2).
L -> F (IN REF. 3).
D -> E (IN REF. 1).
7B3CD198D56DF589 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-UL-1998 (Rel. 36, Last annotation update)
APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
                                                                                                           Pred. No. 4.44e-25;
                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                          192 AA
                                                                                           Score 231;
76 76 C
126 126 C
149 149 L
159 159 D
192 AA; 21350 MW;
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                                                                                         Query Match 16.5%;
Best Local Similarity 27.3%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         BAXA_MOUSE
                                                                                                                                                                                                                                                                                                             152 G 152
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CONFLICT
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GHK -> VGACLVE (IN ISOFORM BCL-2-BETA).
AA85EF6B0766BE0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 VATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!-SUBGELLULAR LOCATION: MITOCHONDRIAL INNER AND OUTER MEMBRANES, AS WELL AS NUCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM.
-!-ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TERMINAL ENDS.
-!-TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!-DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY SPECEPARING THE RELEASE OF CYTOCHROME C. MIGHT FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87
                                                                      SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND BAK PROTEINS, AND WITH BCL-X(S). HETERODIMERIZATION WITH BAX REQUIRES INTACT BH1 AND BH2 DOMAINS, AND IS NECESSARY FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apoptosis; Alternative splicing; Transmembrane; Mitochondrion.
DOMAIN 10 30 BH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 236;
                                                                                                                                                                                                                                                                                                               -:- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-:- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-:- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-:- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
-:- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 VELYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L31532; AAA37282.1; -.
EMBL; M16506; AAA37282.1; JOINED.
EMBL; M16506; AAA37281.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50062; BCL2_FAMILK; 1. PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1. PROSITE; PS01259; BH3; 1. PROSITE; PS01260; BH4_1; 1. PROSITE; PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 AA; 26425 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 45.2%;
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A25960; TVMSA1.
PIR; B25960; TVMSB1.
PIR; E37332; E37332.
HSSP; Q07817; 1MAZ.
MGD; MGI:88138; BCLZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00452; Bcl-2;
                                                                                                                                                                                                                                                                                                       FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 GINWGRIVAFFSFGRALCVESANKEMIDLLPRIVQWMVNYLEHTLQPWMQENGGWEAFVG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 GEGATQGIVEEEVLQALLEATEEFELRYQRAFSDLTSQLHITQDTAQQSFQQVMGELFRD 105
                                                                                                                                                                                                                                                                                                                         -1- FUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.
-1- BUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.
-1- DEVELOWENTAL STAGE: DEVELOWENTAL REGULATION ONLY OCCURS IN THE BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.7%; Score 554; DB 1; Length 204;
47.4%; Pred. No. 6.05e-96;
7ative 28; Mismatches 51; Indels 1; Gaps
                                                                                                                                                                                                                                                           Cruz-Reyes J., Tata J.R.; "Cloning, characterization and expression of two Xenopus bcl-2-like
                                                                                       APOPTOSIS REGULATOR R11 (XR11).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 AA; 23379 MW; 3BFC6BE6DDA4CA03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAXA_RAT STANDARD; PRT; 192 AA. 06360; 062995; 064383; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-FB2-2000 (Rel. 39, Last annotation update) APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 LYGKNAAAQSRESQERFGRLLTIVMLTGVFAL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS50062; BCL2_FAMILX; 1.
PFAM; PF00452; BCL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X82461; CAA57844.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 47.4%;
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apoptosis; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norveqicus (Rat).
   STANDARD;
                                                                                                                                                                                                                                                                                              cell-survival genes.";
Gene 158:171-179(1995)
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          MEDLINE; 95331613.
AR11_XENLA
Q91828;
                                                                                                                                                                                                                          TISSUE-HEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                      Xenopus.
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     SEPTIFICATION
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                                                                          Hockenbery D., Nunez G., Milliman C., Schreiber R.D., Korsmeyer S.J.; "BG1-2 is an inner mitochondrial membrane protein that blocks programmed cell death."; Nature 348:334-336(1990).
                                                                                                                                                                                                                                                                                 -1- FUNCTION: PROLÒNGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE PRESENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPAGES BY PREVENTING THE RELEAGE OF CYTOCHROME C. MIGHT FUNCTION IN AN ANTICXIDANT PATHWAX TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER AND OUTER MEMBRANES, AS WELL AS NUCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM.
-1- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISEASE: INVOLVED IN FOLLICULAR LYMPHOMA (FL) (ALSO KNOWN AS TYPE II CHRONIC LYMPHATIC LEUKEMIA) BY A CHROMOSOMAL TRANSLOCATION T(14;18)(Q32;Q21) WHICH INVOLVES BCL2 AND IMMUNOGLOBULIN GENE
                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND
                                                                                                                                                                                                                                                                                                                                                                                                                                   BAK PROTEINS, AND WITH BCL-X(S). HETERODIMERIZATION WITH BAX REQUIRES INTACT BHI AND BH2 DOMAINS, AND IS NECESSARY FOR ANTI-APOPTOTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TERMINAL ENDS.
TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proto-oncogene; Apoptosis; Alternative splicing; Transmembrane; Mitochondrion; Chromosomal translocation; Polymorphism;
                                                                                                                                                                                   MEDLINE; 94239528.
Yin X.-M., Oltvai Z.N., Korsmeyer J.;
"BH1 and BH2 domains of Bcl-2 are required for inhibition of apoptosis and heterodimerization with Bax.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M13994; AAA51813.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAA29778.1; -. AAD141111.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA35591.1; ALT_SEQ.
AAA35591.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50062; BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS01260; BH4_1; 1. PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                               Nature 369:321-323(1994)
Blood 79:229-237(1992).
                                     SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVHUBC.
C37332.
D37332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00452; Bcl-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVHUB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P53563; 1AF3.
                                                        MEDLINE; 91066924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proto-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M14745;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D37332;
                                                                                                                                                                     MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGIONS
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PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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PIR;
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                                                                                         GHK -> VGASGDVS (IN ISOFORM BCL-2-BETA).
G->A: NO HETERODIMERIZATION WITH BAX, AND
                                                                             DAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLGAYL
                                                                                                                                                                                  P -> S (IN NON-HODGKINS-LYMPHOMA; SOMATIC
                                                                                                                                                                                                                        -> I (IN NON-HODGKINS-LYMPHOMA; SOMATIC
                                                                                                                                                                                                                                                                                                                                                                                         81 AAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELFRD 140
                                                                                                                                                                                                                                                                                                                                                                                                                                            141 GVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAFVE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                        mbcl-2: structure and expression of the murine
human gene involved in follicular lymphoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eguchi Y., Ewert D.L., Tsujimoto Y.; "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in
                                                                                                                                                                                                                                                                                                                                                                  5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   30 GAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adult and embryo.";
Nucleic Acids Res. 20:4187-4192(1992).
-!- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS
                                                                                                                 LOSS OF ANTI-APOPTOTIC ACTIVITY. W->A: NO HETERODIMERIZATION WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rođentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                            LOSS OF ANTI-APOPTOTIC ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BALB/C; TISSUE-LIVER;
MEDLINE; 87187643.
Negrini M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.;
"Molecular analysis of mbcl-2: structure and expression of
gene homologous to the human gene involved in follicular ly
                                                                                                                                                                                                                                                                                                                                        Length 239;
                                                                                                                                                                                                                                                                                                                                                                  44; Mismatches 41; Indels
                                                                                                                                                                                                                                                           I -> F (IN REF. 4).
P -> T (IN REF. 3).
S -> R (IN REF. 3).
R -> C (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 2.68e-103;
                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                /FTId=VAR_000829
                                                                                                                                                                     /FTId=VAR_000827
                                                                                                                                                                                                          /FTId=VAR_000828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P10417; P10418;
01-MAR-1989 (Rel. 10, Created)
01-APR-1993 (Rel. 25, Last sequence update)
101-ML-1998 (Rel. 36, Last annotation update)
APOPTOSIS REGULATOR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 236 AA
                                                                                                                                                                                                                                                                                                                                        Score 586;
                                                                  POTENTIAL
                                                                                                                                                                                                                                    MUTATION)
                                                                                                                                                                                              MUTATION
                                                                                                                                                                                                                                                           48 I
59 P
117 S
129 R
26266 MW;
                                                                                                                                                                                                                                                                                                                                        41.9%;
                                                                                                                                                                                                                                                                                                                                                    Local Similarity 45.1%;
                                                                                                                                                                                                                                                                                                                                                                 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
            30
107
155
202
233
233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                            48
59
117
129 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 92375724.
 Disease mutation
                        93
136
187
212
196
                                                                                                                             188
                                                                                                                                                                                 59
                                                                                                                                                                                                                        63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BCL2 OR BCL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCL2_MOUSE
                                                                                                                                                                                                                                                                       CONFLICT
                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                             VARSPLIC
                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                     MUTAGEN
                                                                                                                               MUTAGEN
                                                                                                                                                        VARIANT
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          DOMAIN
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: TYPOCHONDRIAL INNER AND OUTER MEMBRANES, AS WELL AS NUCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM.
-1- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-FERMINAL ENDS.
-1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES, WITH HIGHEST LEVELS IN REPRODUCTIVE TISSUES. IN THE ADULT BRAIN, EXPRESSION IS LOCALIZED IN MITRAL CELLS OF THE OLFACTORY BULL, GERREBELLAR GRANULE NEURONS OF HIPPOCAMPUS, PONTINE NUCLEI, CERREBELLAR GRANULE NEURONS, AND IN BPENDYMAL CELLS. IN PRENATAL BRAIN, EXPRESSION IS HIGHER AND LOCALIZED IN THE NEUROEPITHELIUM AND IN THE CORFICEAL PLATE.
-1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                               Neuroscience 61:165-177(1994).

**PURCECON: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY PREVENTING THE RELEASE OF CYTOCHROME C. MIGHT FUNCTION IN AN ANTIOXIDARY PARHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.
                                                                         "Inity J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
"Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xhom messenger ribonucieic acid levels.";
Endocrinology 136:232-241(1995).
                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND
                                                                                                                                                                                                                                                                                                                                                                                                                           BAK PROTEINS, AND WITH BCL-X(S). HETERODIMERIZATION WITH BAX REQUIRES INTACT BHI AND BH2 DOMAINS, AND IS NECESSARY FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                    "bcl-2 messenger RNA is localized in neurons of the developing and
                                                                                                                                                                                                      MEDLINE; 95059917.
Castren E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apoptosis; Alternative splicing; Transmembrane; Mitochondrion. DOMAIN 10 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                         STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY; MEDLINE; 95129487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P53563; 1AF3.
PROSITE: P550062; BCL2_FAMILY; 1.
PROSITE: P501080; BH1; 1.
PROSITE: P501258; BH2; 1.
PROSITE; P501259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L14680; AAA53662.1; -. EMBL; U34964; AAA77687.1; -. EMBL; S74122; CAB33200.1; -.
                                                                                                                                                                                       SEQUENCE OF 19-172 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01260; BH4_1; 1. PROSITE; PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00452; Bcl-2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104
152
 Gene 140:291-292(1994)
                                                                                                                                                                                                                                                                     adult rat brain.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION.
                                                                                                                                                                                                                                       Lindholm D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleary M.L., Smith S.D., Sklar J., "Cleary M.L., Smith S.D., Sklar J., "Cloning and structural analysis of cDNAs for bcl-2/immunoglobulin transcript resulting from the t(14;18) translocation.";
                                                                                                                                                                                                                                                                                                        76 VANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
                                                                                                                                                                                                                                                                                                                                                                                                          136 RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Gaps
                                                                                                                                                                                                                                                                                                                                              28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2-Ig fusion gene in lymphoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tsujimoto Y., Croce C.M.; "Analysis of the structure, transcripts, and protein products of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-131 FROM N.A., AND VARIANTS NON-HODGKINS-LYMPHOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILNE; 92096610.

Tanaka S., Louie D.C., Kant J.A., Reed J.C.;

"Frequent incidence of somatic mutations in translocated BCL2 oncogenes of non-Hodgkin's lymphomas.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S.,
                                                                                                                                                                                                         Length 236;
                                                                                                                                                                                                                                                       43; Mismatches 43; Indels
                                                A -> R (IN REF. 2).
E -> G (IN REF. 1).
S -> Y (IN REF. 2).
L -> O (IN REF. 2).
H; E7688CB9071A872A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bcl 2, the gene involved in human follicular lymphoma.";
proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 VELYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 TALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                         Score 586; DB 1; Le
Pred. No. 2.68e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BCL2_HUMAN STANDARD; PRT; 239 AA. P10415; P10416; Q16197; Q13842; Q1-MAR-1989 (Rel. 10, Created) Clark-1989 (Rel. 25, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update)
     BH2.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 20:4187-4192(1992).
                                                                                                                                                                                                                                    Pred.
199 BH
230 PC
42 A
157 E
164 S
212 L
26622 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goldman P., Korsmeyer S.J.;
                                                                                                                                                                                                            41.98;
                                                                                                                                                                                                                                    Best Local Similarity 45.2%;
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APOPTOSIS REGULATOR BCL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 7:123-131(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell 47:19-28(1986).
                                                                                                                             212
236 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 86259760.
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                                                   CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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                             TRANSMEM
                                                                                                                                                                                                            Query Match
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Cazals-Hatem D.L., Loule D.C., Tanaka S., Reed J.C.;

"Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue of toning and DNA sequence analysis of cDNA encoding chicken homologue of the Ed. 2 oncoprotein.";

Biochim. Blophys. Acta 1132:109-113(1992).

-! FUNCTION: PROUINED GROWTH FACTORS AND ALSO IN THE PRESENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF WARIOUS STIMULI INDUCING CELULAR DEATH. BCLZ BLOCKS APOPTOSIS BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY PREVENTING THE RELEASE OF CYTOCHROME C. MIGHT FUNCTION IN AN ANTIOXIDAMY PATHWAY TO PREVENT ACTIVATION OF CASPASES BY PREVENTING THE RELEASE OF CYTOCHROME C. MIGHT FUNCTION IN AN ANTIOXIDAMY PATHWAY TO PREVENT ACTIVATIVY).

-! SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND BAX PROTEINS. HETERODIMERIZATION WITH BAX REQUIRES INTACT BHI AND STATES AND IS NECESSARY FOR ANTI-APOPTOTIC ACTIVITY (BY STATES AND ACT
                                                                                                                                                                                                                                                                                                                                                    'n
                                                                                                                           FSRK -> VRTTPLVCPPLACVSLLCEHP (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                          MISSING (IN ISOFORM BCL-X(S)).
DTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSI
                                                                                                                                                                      LYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSLFSRK
                                                                                                                                                                                                  -> GHDCGWCGSAGLTLQSEVTRH (IN ISOFORM BCL.
                                                                                                                                                                                                                                                                                                                                                                                             85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
                                                                                                                                                                                                                                                                                                                                                                                                                          101 LFGAALCAESVNKEMEPLVGQVQEMMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 92375724.

Eguchi Y., Ewert D.L., Tsujimoto Y.;

"Isolation and characterization of the chicken bol-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: MITOCHONDRIAL INNER AND OUTER MEMBRANES, AS
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILAKITY).
-1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                                    5,
                                                                                                                                                                                                                                                                                                 DB 1; Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WELL AS NUCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM (BY
                                                                                                                                                                                                                                                                                                                                                  30; Mismatches 36; Indels
                                                                                                                                                                                                                                                24D2AC79887E072E CRC64;
                                                                                                                                                                                                                                                                                                 Score 615; DB 1; LA Pred. No. 5.42e-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
10-APR-1993 (Rel. 25, Last sequence update)
10-LUL-1998 (Rel. 36, Last annotation update)
APOPTOSIS REGULATOR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 AA
                                                                                                                                                                                                                            X(DELTA-TM))
                                                                                                                                                    BCL-X-BETA)
                                                     POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 KGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26132 MW;
                                                                                                                                                                                                                                                                                                 44.0%;
                                                                                                                                                                                                                                                                                                                        Best Local Similarity 53.1%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BCL2 OR BCL-2.
Gallus gallus (Chicken).
  148
195
226
188
233
                                                                                                                                                                                                                                                233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 92379084.
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  129
180
210
126
189
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                                              TRANSMEM
VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                         VARSPLIC
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  DOMAIN
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-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 PAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVEELFRDG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 VNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGWDAFVEL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-BRAIN;
BUDLINE; 94193015.
Sato T., Irie S., Krajewski S., Reed J.C.;
"Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E -> S (IN REF. 2).
GSAAASEVPPAEGLRP -> ARLLLVRCPRLRGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 233;
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
-i- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IN REF. 2).
H -> T (IN REF. 2).
G -> V (IN REF. 2).
5252555ACB6E4C3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 YGN-SM---RPLFDFSWISLKTILS-LVLVGACITLGAYLGHK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 587; DB 1; Le Pred. No. 1.57e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLL2_RAT

P49950; Q62837; Q64032;

01-OCT-1996 (Rel. 34, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41; Mismatches
                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   Apoptosis; Transmembrane; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                        PIR; A7332; A7332.
PIR; S24390; S24390.
HISSP; P53563; 1AF7.
PROSITE; PS010062; BCL2_FAMILY; 1.
PROSITE; PS012080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4_1; 1.
                                                                                                                                                                                               EMBL; D11382; BAA01978.1; -.
EMBL; D11381; BAA01978.1; JOINED.
EMBL; Z11961; CAA78018.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25687 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 42.0%;
Best Local Similarity 46.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APOPTOSIS REGULATOR BCL-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
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196
228
64
82
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                                                                                                                                                                                                                                                                                                                                                                                                                                              130
181
208
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THE STANTANT OF THE STANT OF TH
                                                                                                                                                                  MISSING (IN ISOPORM BCL-X(S)).
DTFVDLYGNNAAAESRKGGERFNRWELTGMTVAGVVLLGSL
FSRK -> VRTTPLVCPPLVCLSSVEEPNCFWSPGNVED
IDYSGDIPGLL (IN ISOFORM BCL-X(BETA)).
R -> G (IN REF. 2).
A -> E (IN REF. 2).
A -> E (IN REF. 4).
A -> V (IN REF. 4).
FF -> SS (IN REF. 4).
A -> V (IN REF. 4).
A -> T (IN REF. 4).
A -> T (IN REF. 4).
A -> P (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gonzalez-Garcia M., Perez-Ballestero R., Ding L., Duan L., Boise L.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 LFGAALCAESVUKEMEPLVGQVQEMMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
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Fang W., Rivard J.J., Mueller D.L., Behrens T.W.;
"Cloning and molecular characterization of mouse bcl-x in B and T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                PFMM; PF00452; BG1-2; 1. Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thompson C.B., Nunez G.; Thompson C.B., Nunez G.; The major bcl-x mRNA form expressed during murine development and its product localizes to mitochondria."; Development 120:3033-3042(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.0%; Score 615; DB 1; Length 233 larity 53.1%; Pred. No. 5.42e-110; Conservative 30; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (X(L); X(S) AND X(DELTA-TM) ISOFORMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ramesaki H., Michaud G.Y., Takatsu K., Okuma M.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BCLX_MOUSE STANDARD; PRT; 233 AA. 064373; 060657; 060658; 061338; 01-NOV-1997 (Rel. 35, Created) PLINOV-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (X(L) AND BETA ISOFORMS).
STRAIN-C57BL/6; TISSUE=BRAIN;
MEDLINE; 95331139.
                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 KGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lymphocytes.";
J. Immunol. 153:4388-4398(1994).
                                                                                                                                                                                                                                                                                                                                                                                        201 A
26158 MW;
  PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APOPTOSIS REGULATOR BCL-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BCL2L1 OR BLC2L OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                               119
143
199
201
233 AA;
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ses 77; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                        3D-structure.
DOMAIN
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CONFLICT
CONFLICT
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SEQUENCE
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TRANSMEM
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  PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEVELOPMENTAL STAGE: BCL-X(BETA)IS EXPRESSED IN BOTH EMBRYONAL AND POSTNATAL TISSUES, WHEREAS BCL-X(L) IS PREDOMINANTLY FOUND IN POSTNATAL TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                    Genillot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N.,
Ohta S., Seldin M.F., Nunez G.;
"Genomic organization, prometer region analysis, and chromosome
localization of the mouse bcl-x gene.";
J. Immunol. 158.4750-4757(1997).
-!-FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
FORM AND THE DELTA-TH FORM DISPLAY CELL DEATH REPRESSOR ACTIVITY,
WHEREAS THE SHORT ISOPORM PROMOTES APOPTOSIS (BY SIMILARITY).
-!- SUBUNIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAX, WHEREAS
BCL-X(S) FORMS HETERODIMERS WITH BAX AND BAX, WHEREAS
BCL-X(S) FORMS HETERODIMERS WITH BAX AND BAX, WHEREAS
BAX DOES NOT SEEM TO BE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE FOR BCL-X(L). CYTOPLASMIC FOR BCL-X(DELTA-TM).
ALTERNATIVE PRODUCTS: FOUR ISOFORMS, BCX-X(L) (SHOWN HERE), BCL-X(S), BCL-X-BETA AND BCL-X(DELTA-TM), ARE DERIVED BY ALTERNATIVE PLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN THE BRAIN, THYMUS, BONE MARROW, AND KIDNEY. BCL.X(L) AND BCL.X(DELTATM) EXPRESSION IS ENHANCED IN B AND T LYMPHOCYTES THAT HAVE BEEN ACTIVATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                             Yang X.-F., Weber G.F., Cantor H.; A novel Bol.x isoform connected to the T cells responsis in T cells." Immunity 7:629-639(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apoptosis; Mitochondrion; Alternative splicing; Transmembrane. DOMAIN 4 24 BH4. DOMAIN 86 100 BH3.
                                                          STRAIN-C57BL/6 X CBA; TISSUE-THYMUS;
MEDLINE; 98051053.
[4]
SEQUENCE FROM N.A. (BETA ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50062; BCL2_FAMILY; 1. PS01080; BH1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U78031; AAB96881.1; -.
EMBL; U78030; AAB96881.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X83574; CAA58557.1; -.
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PROSITE; PS01260; BH4_1; 1.
PROSITE; PS50063; BH4_2; 1.
PFAM; PF00452; BC1-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:88139; BCL2L.
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                                                                                                                                                                                                                                                                                                  [5]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 97289584.
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PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE;
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SEQUENCE FROM N.A. (X(L) AND X(S) ISOFORMS)

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POTENTIAL.
EREVDLYGNNAAAELRKGQETFNKWLLTGATVAGVLLLGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 ASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFHDGVNWGRIVA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 FFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWERFVDLYGNNAAAE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
-1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE (BY SIMILARITY).
-1- ALTERNATIVE PRODUCTS: A LONG ISOFORM (SHOWN HERE) AND A SHORT ISOFORM ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOID
                                                                                      DEVELOPMENT.

-1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY).

-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).

-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).

-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).

-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSRK -> VRTALP (IN SHORT ISOFORM) 229 AA; 25733 MW; A97D3A4D04C0E9DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 615; DB 1; Length 229;
Pred. No. 5.42e-110;
30; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BCLX_RAT STANDARD; PRT; 233 AA. PF53563; Q62678; P70614; P70614; P70614; Q621836; Q64087; Q64128; Q1-CCT-1996 (Rel. 34, Created) O1-NOV-1997 (Rel. 35, Last sequence update) O1-NOV-1997 (Rel. 35, Last annotation update) BCL2L1 OR BLC2L OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apoptosis; Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 LRKGQETFNKWLLTGATVAGVLLLGSLLS 227
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, 223110; CAA80657.1; --
EMBL, U26645, AA807677.1; --
EMBL, 447537, A47537.
HSSP, P53563; 1AF3.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01259; BH4, 1; 1.
PROSITE; PS01260; BH4, 1; 1.
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ilarity 52.3%;
Conservative
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223
229
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nes 78; Conserv
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                                                                                                                                                                                                                                                                                                                                          Ohta S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENVELOPE (BY SIMILARITY).

-!- ALTERNATIVE PRODUCTS: THREE ISOFORMS, BCL-X(L) (SHOWN HERE),
BCL-X(S) AND BCL-X(BETA), ARE DERIVED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS
SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE
OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DETECTABLE LEVEL OF BCL.X(S).

-!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY).

-!- SIMILARITY: CONTAINS A BCL-2 HOWOLOGY DOMAIN 1 (BH1).

-!- SIMILARITY: CONTAINS A BCL-2 HOWOLOGY DOMAIN 3 (BH2).

-!- SIMILARITY: CONTAINS A BCL-2 HOWOLOGY DOMAIN 3 (BH3).

-!- SIMILARITY: CONTAINS A BCL-2 HOWOLOGY DOMAIN 4 (BH4).

-!- SIMILARITY: CONTAINS A BCL-2 PAMILY.
                                                                                                           Wesselingh S.L., David G.L., Choi S., Veliuona M., Hardwick J.M.; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
                                                                                                                                                                                                           Shiraiwa N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Oh
"An additional form of rat Bcl-x, Bcl-xbeta, generated by an
unspliced RNA, promotes apoptosis in promyeloid cells.";
J. Biol. Chem. 271:13258-13265(1996).
                                            Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (X(L) AND X(S) ISOFORMS). STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY;
                                                                                                                                                               SEQUENCE FROM N.A. (X(L) AND BETA ISOFORMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S76513; AAC60701.1; ALT_INIT.
S78284; AAC60702.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50062; BCL2_FAMILY; 1. PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1. PROSITE; PS01259; BH3; 1. PROSITE; PS01260; BH4_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, X82537; CAA57886.1; -.
EMBL, X82537; CAA57887.1; -.
EMBL, U10579; AAA19257.1; -.
EMBL, U7250; AAB17353.1; -.
EMBL, U72349; AAB17352.1; -.
EMBL, U34963; AAA77686.1; -.
                                                                                                                                                                                             MEDLINE; 96278736.
                                                                                                                                                                                                                                                                                                                              MEDLINE; 95129487.
                                                                              SEQUENCE FROM N.A.
                              Michaelidis T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
                                                                                                                                                                                TISSUE=THYMUS
               ISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1AF3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C. I- SUBUNIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS THE SHORT ISOFORM PROMOTES APOPTOSIS.

C. I- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT ISOFORM PROMOTES APOPTOSIS.

C. I- SUBUNIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS BCL-X(S) FORMS HETERODIMERS WITH BCL-2. HETERODIMERIZATION WITH BAX DOES NOT SEEM TO BE REQUIRED FOR AWII-APOPTOTIC ACTIVITY.

C. I- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPEE (BY SIMILARITY).

C. I- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPEE (BY SIMILARITY).

C. I- TISSUES SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS.

C. I- TISSUES SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS.

C. I- TISSUES OF A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING

LIMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING

C. I- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANIT- APOPTOTIC

FUNCTION: INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANII-

C. I- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANIT-

C. I- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANIT-

C. I- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANIT-

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C. ADOM
                 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 96256675.

MUChmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,
Yoon H.S., Nettesheim D., Chang B.S., Thompson C.B., Wong S.L.,
Ng S.L., Reslat S.W.;
X-ray and NMR structure of human Bcl-xL, an inhibitor of programmed cell death.";
                                                                                                                                                                                                             MEDLINE; 96170038.
Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M.,
Korsmeyer S.J.;
                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE BY NMR OF 1-209.
MEDLINE; 97172562.
Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J.E.,
Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
Thompson C.B., Fesik S.W.;
Thompson G.B., Fesik S.W.;
"Structure of Bcl.*XL-Bak peptide complex: recognition between
regulators of apoptosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
--- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
---- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
---- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
---- SIMILARITY: GDATAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                          "Bax-independent inhibition of apoptosis by Bcl-XL.";
Nature 379:554-556(1996).
                                                                                                                       roc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995)
                                                                                                                                                                                 MUTAGENESIS OF BH1 AND BH2 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS50062; BCL2_FAMILY; 1.
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EMBL; Z23115; CAA80661.1; -.
EMBL; U72298; AAB1734.1; -.
PDB; 1BXL; 29-OCT-97.
PDB; 1LXL; 21-APR-97.
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BH2; 1.
BH3; 1.
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PROSITE; PS01258;
PROSITE; PS01259;
MEDLINE; 95372373.
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Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus
                                                                                                                                                                                                                                                           DTFVELYGNNAAAESRKGGERPNRWFLTGMTVAGVVLLGSL
FSRK -> VRTKPLVOPFSLASGORSPTALLLLLLLLCWVI
VGDUDS (IN ISOFORM BCL-X(BETA)).
FRD-YNRA: NO HETERODIMERIZATION WITH BAX.
VNW->AIL: LOSS OF ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T., Turka L.H., Mao X., Nunez G., Thompson C.B.;
"bcl.x, Mao Larelated gene that functions as a dominant regulator of apoptotic cell death.";
cell 74:597-608(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPICOL. Dev. 47:26-29(1997).
FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT
                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVITY.

G->A: NO HETERODIMERIZATION WITH BAX.

G->E: NO HETERODIMERIZATION WITH BAX.
                                 PFAM; PF00452; BCl-2; 1.
Apoptosis; Mitochondrion; Alternative splicing; Transmembrane; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                               GRI->ELN: LOSS OF ANTI-APOPTOTIC ACTIVITY.
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                                                                                                                                                                                                                                      MISSING (IN ISOFORM BCL-X(S)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 616; DB 1; Length 233;
Pred. No. 3.18e-110;
30; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G -> A (IN CAA80661).
E09D3CDD851AE9BE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        00-816; 098908;
01-FEB-1995 (Rel. 31, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
BCL2L1 OR BCLAR BCLAR.
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STRAIN-HUBBARD WHITE MOUNTAIN; TISSUE-TESTIS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (SHORT FORM). MEDLINE; 93364977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26049 MW;
PROSITE; PS01260; BH4_1; 1. PROSITE; PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 44.1%;
Local Similarity 53.1%;
Les 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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148
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129
180
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148
188
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TRANSMEM
VARSPLIC
VARSPLIC
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                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myocardium of pig."; to the EMBL/GenBank/DDBJ databases.

-!-Formating and stunned
Submitted (JAN-1998); to the EMBL/GenBank/DDBJ databases.

-!-FONCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT AND
THE BETA ISOFORMS PROMPTE APOPTOSIS.

-!- SUBUNIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS
BCL-X(S) FORMS HETERODIMERS WITH BCL-2. HETERODIMERIZATION WITH
BAX DOES NOT SEEM TO BE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 LETNLRDWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGALMTVGAL 224
                                                                                                                                                                                                                                                                                                                                                                                                      48 SRALVEDLVRYKLCQRSLV - PEPS - GAASCALHSAMRAAGDEFEERFRQAFSEISTQIH 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 VTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDWMVTY 164
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
"Expression of apoptosis-associated genes in hibernating and stunned
                                                                                                                                                                                                                                                                                                                                                                              3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE (BY SIMILARITY).

DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                Score 931; DB 1; Length 228; Pred. No. 3.73e-184;
 -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
                                                                                                                                                                                                                                                                                                                                                                              35; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                  228 AA; 25068 MW; C499D449A585F8A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
BCL2L1 OR BLC2L OR BCLX.
                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                   PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01058; BCL2_FAMILY; 1.
PFAM; PF00452; BCl-2; 1.
Apoptosis; Transmembrane.
                                                                                                                                                            EMBL; X82462; CAA57845.1; -.
                                                                                                                                                                                                                                                                                                                                                                         Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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SEQUENCE
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077737;
                                                                                                                                                                                                                                                            NON_TER
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVLNELFRDGVNWGRIVAFF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 SFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T., Turka L.A., Mao X., Nunez G., Thompson C.B.;
"bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic cell death.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 233;
APOPTOTIC ACTIVITY (BY SIMILARITY).

-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).

-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).

-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).

-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).

-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inohara N., Ohta S.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 100 BH3.
129 148 BH1.
180 195 BH2.
210 226 POTENTIAL.
233 AA: 26061 MW; 18BF6FA0441912B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 618; DB 1; Lo
Pred. No. 1.10e-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               007817; 092976;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (X(L) AND X(S) ISOFORMS).
                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50062; BCL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4_1; 1.
PROSITE; PS50063; BH4_2; 1.
PFAM; PF00452; BCl-2; 1.
Apoptcsis; Mitochondrion; Transmembrane.
DOMAIN 86 100 BH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 KGQERFNRWFLTGMTLAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 RLREG-N-WASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (BETA ISOFORM).
                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ001203; CAA04597.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 44.2%;
Local Similarity 53.8%;
es 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APOPTOSIS REGULATOR BCL-X. BCL2L1 OR BLC2L OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 93364977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCLX_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
                                                                                                                                                                                                                                                                                               9 29 BH4.
85 104 BH1.
136 151 BH2.
193 AA; 20774 MW; 3792243A50281761 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1383; DB 1; Pred. No. 2.09e-292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                               PROSITE; PS50062; BCL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01260; BH4_1; 1.
PROSITE; PS01260; BH4_1; 1.
PROSITE; PS50063; BH4_2; 1.
                  EMBL; U59747; AAB09055.1; -. EMBL; D87461; BAA19666.1; -. HSSP; P53563; IAF3. MIN; 601931; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               99.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APOPTOSIS REGULATOR BCL-W. BCL2L2 OR BCLW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND SALIVARY GLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GALVTVGAFFASK 193
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SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 96358615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/10J;
MEDLINE; 98160183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 2
BCLW_MOUSE
P70345;
                                                                                                                                                                                                                                                                          Apoptosis.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
CCC DR DDR DDR CCC DR CCC DR CCC DR CCC DDR CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
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                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MATPASTPDIRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OLINOY-1997 (Rel. 35, Created)
01-NOY-1997 (Rel. 35, Last sequence update)
01-NOY-1997 (Rel. 35, Last annotation update)
APOPTOSIS REGULATOR R1 (RT1) (FRAGMENT).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopoodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 193;
-:- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 29 BH4.
85 104 BH1.
136 151 BH2.
193 AA; 20790 MW; 36CA185F5945DFB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1380; DB 1;
Pred. No. 1.10e-291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 AA
                                                                                                                                                                                                                                                                                                                                                                                               MGD; MCI:108052; BCL2L2.
PROSITE; PS50062; BCL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01268; BH4_1; 1.
PROSITE; PS501260; BH4_1; 1.
PROSITE; PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                               EMBL; U59746; AAB09056.1; -.
EMBL; AF030769; AAB86430.1;
HSSP; P53563; IAF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 97.9%;
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 GALVTVGAFFASK 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=HEAD;
MEDLINE; 95331613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AR1_XENLA
Q91827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apoptosis.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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           SO THE FET THE DESCRIPTION OF THE PROPERTY OF 
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protein · protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Jun 23 14:14:40 2000; MasPar time 7.84 Seconds 749.617 Million cell updates/sec Run on:

Tabular output not generated

>US-09-155-327B-7 (1-193) from US09155327B.pep 1397 Description: Perfect Score:

1 MATPASAPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193 Sequence:

PAM 150 Gap 11 Scoring table:

83857 segs, 30454973 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

1:swissprot swiss-prot38 Database:

Mean 46.104; Variance 80.361; scale 0.574 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Pred. No.                     | 2.09e-292            | 1.10e-291            | 3.73e-184           | 1.10e-110          | 3.18e-110            | 5.42e-110            | 5.42e-110          | 5.42e-110            | 1.57e-103            | 2.68e-103          | 2.68e-103            | 7.73e-103            | 6.05e-96             | 4.44e-25           | 4.44e-25             | 1.12e-24             | 1.78e-24               | 1.78e-24               | 4.50e-24         | 7.14e-24         | 1.79e-22               | 6.86e-21               | 1.15e-15               |
|-------------------------------|----------------------|----------------------|---------------------|--------------------|----------------------|----------------------|--------------------|----------------------|----------------------|--------------------|----------------------|----------------------|----------------------|--------------------|----------------------|----------------------|------------------------|------------------------|------------------|------------------|------------------------|------------------------|------------------------|
| Description                   | OSIS REGULATOR BC    | OSIS REGULATOR BC    | OSIS REGULATOR R1   | OSIS REGULATOR BC  | OSIS REGULATOR BC    | OSIS REGULATOR BC    | OSIS REGULATOR BC  | OSIS REGULATOR BC    | OSIS REGULATOR BC    | OSIS REGULATOR BC  | OSIS REGULATOR BC    | OSIS REGULATOR BC    | OSIS REGULATOR R1    | OSIS REGULATOR BA  | OSIS REGULATOR BA    | OSIS REGULATOR BA    | BAX PROTEIN, CYTOPLASM | APOPTOSIS REGULATOR BA | HOMOLOGOUS ANTAG | HOMOLOGOUS ANTAG | APOPTOSIS REGULATOR BA | BCL-2 HOMOLOGOUS ANTAG | APOPTOSIS REGULATOR NR |
| Descr                         | BCLW_HUMAN APOPTOSIS | BCLW_MOUSE APOPTOSIS | AR1_XENLA APOPTOSIS | BCLX_PIG APOPTOSIS | BCLX_HUMAN APOPTOSIS | BCLX_CHICK APOPTOSIS | BCLX_RAT APOPTOSIS | BCLX_MOUSE APOPTOSIS | BCL2_CHICK APOPTOSIS | BCL2_RAT APOPTOSIS | BCL2_HUMAN APOPTOSIS | BCL2_MOUSE APOPTOSIS | AR11_XENLA APOPTOSIS | BAXA_RAT APOPTOSIS | BAXA_MOUSE APOPTOSIS | BAXA_BOVIN APOPTOSIS | BAXD_HUMAN BAX P       | BAXA_HUMAN APOPT       | 3AK_HUMAN BCL-2  | 3AK2_HUMAN BCL-2 | BAXB_HUMAN APOPT       |                        | NR13_COTJA APOPTO      |
| DB ID                         | 1 BCL                | 1 BCL                | 1 AR1               | 1 BCL              | 1 BCL                | 1 BCL                | 1 BCL              | 1 BCL                | 1 BCL                | 1 BCL              | 1 BCL                | 1 BCL                | 1 AR1:               | 1 BAX              | 1 BAX                | 1 BAXI               | 1 BAXI                 | 1 BAX                  | 1 BAK            | 1 BAK            | 1 BAXE                 | 1 BAK                  | 1 NR1                  |
| %<br>Query<br>Match Length DB |                      |                      |                     | 2 233              | 1 233                | 0 229                | 0 233              |                      |                      |                    |                      |                      |                      | 5 192              |                      |                      | 3 143                  |                        |                  |                  |                        | •                      | 177                    |
| :                             |                      | 80 98.8              |                     | 618 44.            | 616 44.              | -                    | •                  |                      |                      |                    |                      |                      |                      | 1 16.5             |                      |                      |                        |                        |                  |                  |                        |                        | 3 13.1                 |
| ult<br>No. Score              | 1 1383               | 2 1380               | 3 931               | 4 61               | 5 61                 | 6 61                 |                    | 8 615                |                      | 10 586             |                      |                      | 13 55                | 14 231             | 15 23                |                      |                        | 18 22                  |                  |                  |                        | 22 21                  | 23 18                  |
| Result<br>No.                 |                      |                      |                     |                    |                      |                      |                    |                      |                      |                    |                      |                      |                      |                    |                      |                      |                        |                        |                  |                  |                        |                        |                        |

| 1.11e-10               | 1.68e-10               | 1.95e-09               | 1.30e-09               | 2.93e-09               | 2.38e-06               | 3.49e-06               | 3.49e-06               | 2.93e-01               | 7.61e-01               | 1.42e+00              | 1.04e+00                | 1.42e+00               | 1.04e+00               | 1.04e+00               | 1.04e+00               | 1.93e+00               | 1.93e+00              | 1.93e+00               | 1.93e+00               | 1.93e+00              | 1.93e+00               |
|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|-----------------------|-------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|-----------------------|------------------------|------------------------|-----------------------|------------------------|
| APOPTOSIS REGULATOR CE | BCL2-RELATED PROTEIN A | BCL2-RELATED PROTEIN A | INDUCED MYELOID LEUKEM | APOPTOSIS REGULATOR CE | APOPTOSIS REGULATOR BC | APOPTOSIS REGULATOR BC | APOPTOSIS REGULATOR BC | NODULATION PROTEIN NOL | HYPOTHETICAL 67.1 KD P | LIGNINASE C PRECURSOR | GLUCAN 1, 3-BETA-GLUCOS | DNA-DAMAGE-INDUCIBLE P | GAG POLYPROTEIN [CONTA | PROBABLE ABC TRANSPORT | LOW-DENSITY LIPOPROTEI | HYPOTHETICAL 36.5 KD P | L-ARABINOSE ISOMERASE | MYOCYTE-SPECIFIC ENHAN | COMPETENCE PROTEIN COM | PULLULANASE PRECURSOR | PUTATIVE HELICASE HELY |
| CED9 CAEBR             | BFL1_MOUSE             | BFL1_HUMAN             | MCL1_HUMAN             | CED9_CAEEL             | EAR_ASFE4              | EAR_ASFM2              | EAR_ASFB7              | NOLO_RHISN             | YH70_SYNY3             | LIGC_TRAVE            | EXG_YARLI               | DINF_ECOLI             | GAG_HV2G1              | Y4FN_RHISN             | LRP1_CHICK             | YHZ8_YEAST             | ARAA_SALTY            | MEFD_HUMAN             | COMA_NEIGO             | PULA_THEMA            | HELY_MYCTU             |
| -                      | Н                      | Н                      | Н                      | -                      | ٦                      | -1                     | H                      | Н                      | Н                      | Н                     | -                       | -                      | Н                      | -1                     | -                      | Н                      | Н                     | Н                      | -                      | Н                     | П                      |
| 271                    | 172                    | 175                    | 350                    | 280                    | 179                    | 179                    | 179                    | 680                    | 585                    | 372                   | 421                     | 459                    | 522                    | 269                    | 4543                   | 321                    | 200                   | 521                    | 691                    | 843                   | 906                    |
| 11.2                   | 11.1                   | 10.7                   | 10.7                   | 10.6                   | 9.4                    | 9.3                    | 9.3                    | 7.0                    | 6.8                    | 6.7                   | 6.7                     | 6.7                    | 6.7                    | 6.7                    | 6.7                    | 9.9                    | 9.9                   | 9.9                    | 9.9                    | 9.9                   | 9.9                    |
| 156                    | 155                    | 149                    | 150                    | 148                    | 131                    | 130                    | 130                    | 86                     | 95                     | 93                    | 94                      | 93                     | 94                     | 94                     | <b>6</b>               | 85                     | 92                    | 92                     | 92                     | 92                    | 85                     |
| 24                     | 25                     | 26                     | 27                     | 28                     | 29                     | 30                     | 31                     | 32                     | 33                     | 34                    | 32                      | 36                     | 37                     | 38                     | 39                     | 40                     | 41                    | 42                     | 43                     | 44                    | 45                     |

## ALIGNMENTS

| RES | RESULT 1<br>ID BCLW HUMAN  | STANDARD:  | PRT:       | 193 AA.   |      |
|-----|----------------------------|--|------------|---|------|
| A C | 092843;                    | ,  | , T        |   |      |
| DŢ  | 01-NOV-1997 (F             | 01-NOV-1997 (Rel. 35, Created)                   | (þ;        |   |      |
| 텀   | 01-NOV-1997 (F             | Rel. 35, Last s                                  | sednence 1 | npdate)   |      |
| ΔĪ  | 01-NOV-1997 (F             | Rel. 35, Last a                                  | nnotation  | n update)   |      |
| DE  | APOPTOSIS REGU             | APOPTOSIS REGULATOR BCL-W (KIAA0271).            | (IAA0271)  |   |      |
| S   | BCL2L2 OR BCLW.            | -  |            |   |      |
| SO  | Homo sapiens (Human).      | Human).  |            |   |      |
| ႘   | Eukaryota; Met             | azoa; Chordata                                   | ı; Craniat | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;         |      |
| ဗ   | Eutheria; Prin             | Eutheria; Primates; Catarrhin1; Hominidae; Homo. | .n1; Homir | idae; Homo.   |      |
| RN  | [1]                        |  |            |   |      |
| КP  | SEQUENCE FROM N.A.         | N.A.   |            |   |      |
| КX  | MEDLINE; 96358615.         | 1615.  |            |   |      |
| RA  | Gibson L., Hol             | .mgreen S.P., H                                  | luang D.C. | Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,     |      |
| RA. | Jenkins N.A.,              | Sutherland G.F                                   | 1., Baker  | E., Adams J.M., Cory S.;  |      |
| RŢ  | "bcl-w, a nove             | al member of th                                  | le bcl-2 f | "bcl-w, a novel member of the bcl-2 family, promotes cell survival."; | 1."; |
| RL  | Oncogene 13:665-675(1996). | 5-675(1996).                                     |            |   |      |
| RN  | [2]                        |  |            |   |      |
| RP  | SEQUENCE FROM N.A.         | N.A.   |            |   |      |
| 2   | TISSUE-BRAIN;              |  |            |   |      |
| X   | MEDLINE; 97191544.         | 544.   |            |   |      |
| RA  | Nagase T., Sek             | i N., Ishikawa                                   | KI., C     | Naqase T., Seki N., Ishikawa KI., Ohira M., Kawarabayasi Y.,          |      |
| RA  | Ohara O., Tana             | ıka A., Kotani                                   | H., Miya   | ima N., Nomura N.;  |      |
| RT  | "Prediction of             | the coding se                                    | duences    | f unidentified human genes.   | VI.  |
| RT  | The coding seq             | nences of 80 n                                   | ew denes   | (KIAA0201-KIAA0280) deduced   | ρΛ   |
| RŢ  | analysis of cb             | NA clones from                                   | cell 11n   | analysis of cDNA clones from cell line KG-1 and brain.";              | •    |
| RL  | DNA Res. 3:321-329(1996).  | 329(1996).                                       |            |   |      |
|     |                            |  |            |   |      |

-!- FUNCTION: PROMOTES CELL SURVIVAL. -!- SUBCELLULAR LOCATION: CYTOPLASMIC

-i- SUBCELLULAR LOCATION: CYTOPLASMIC.
-i- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON, AND SALIVARY GLAND.
-i- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC

8888888888888888888888888

-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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76; Conservative

Matches

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Claim 2: Pages 25-26; 30pp; English.

The present sequence represents "Deprenyl" (RTM)-induced protein (DIP), an ovel protein in neural cells. This protein is induced by the neuroactive drug "Deprenyl" (RTM). DIP 1 and compounds which modulate its activity can be used for the diagnosis and treatment of neuroapoptosis; passociated with diseases such as Alzheimer's, Parkinson's and Huntington's, as well as cerebellar degeneration and oligodendrocyte sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6: Page 46: 75pp; English.

Craim 6: Page 46: 75pp; English.

Craim 6: Page 46: 75pp; English.

Craim 6: Page 46: 75pp; English.

Dlocking or suppressing NF-kappa B (NF-kB) activation. A claimed method of genetically modifying a mammalian endothelial cell to method of genetically modifying a mammalian endothelial cell to cender it less susceptible to an inflammatory or other immunological stimulus comprises inscring into the cell; DNA encoding an anti-apoptotic protein able to inhibit NF-kB, and capperssing the cell such that NF-kB activation of the cell; DNA inhibited in the presence of the the cellular activating stimulus.

Sultable anti-apoptotic proteins include A20 (see W31528), BCL-2

C (see W31529), BCL-XL and A1 (see W3151) and their deletion mutants capable of inhibiting NF-kB, such as polypeptides comprising amino cald residues 5-24, 86-100, 129-148 and 180-195 of BCL-XL. Also cald are: (7), a mammalian endothelial cell modified by the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 623; DB 1; Length 225;
Pred. No. 1.06e-47;
34; Mismatches 32; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant endothelial cell containing DNA encoding anti-apoptotic protein - is less susceptible to inflammatory response and is useful for generating tissues or organs for transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human anti-apoptotic BCL-XL protein.
BCL-XL; anti-apoptotic protein; human; nuclear factor-kappa B;
NF-kappa B; inhibitor; organ transplant; tissue transplant;
inflammation; gene therapy; endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mammal comprising DNA encoding an anti-apoptotic protein of a different species. The method can be used to generate donor endothelial cells or graftable tissues or organs for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         method: and (2) a non-human transgenic or somatic recombinant
   especially by rescuing cells from apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-A0C-1997.
13-FEB-1997; EO0676.
19-FRB-1996; US-634995.
14-FEB-1996; US-601515.
(NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
(NOVS ) NOVARTIS AG.
Bach FH, Ferran C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transplantation into recipient species. Sequence 233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 KGQERFNRWFLTGMTVAGVVLLGSL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W31530 standard; Protein; 233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 52.4%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-FEB-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
WO9730083-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W31530;
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g
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Score 623; DB 1; Length 233; Pred. No. 1.06e-47;

Ouery Match Best Local Similarity 52.4%;

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ë
                          85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
                                        145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
  3; Gaps
34; Mismatches 32; Indels
                                                                                                                                                                                                     Search completed: Fri Jun 23 14:17:53 2000 Job time: 12 secs.
                                                                                                                                   205 KGQERFNRWFLTGMTVAGVVLLGSL 229
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Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and degenerative diseases.

Or inhibit cell survival, e.g. for treatment of cancer and degenerative diseases.

Claim 6; Page 50-51; 86pp; English.

Claim 6; Page 50-51; Page 50-51; 86pp; English.

Claim 6; Page 50-51; 86p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                               Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       viable in culture for an extended period. In contrast, if they act as cell death stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites.
Sequence 192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                           2 PTPASTPDTRALVADEVGYRLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRTF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse bcl-w protein.
Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                  1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGGGPAADPLHQAMRAAGDEFETRFRRTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 7.82e-108;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                  Length 192;
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                     Score 1326; DB 1; I
Pred. No. 7.33e-117;
8; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams JM, Cory S, Gibson LM, Holmgreen SP; WPI; 97-489635/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMRA-) AMRAD OPERATIONS PTY LTD.
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W36048 standard; Protein; 168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis; degenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 Match 89.1%;
Local Similarity 100.0%;
Pes 168; Conservative
                                                                                                                                                                                                                                     95.7%;
Local Similarity 94.3%;
les 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-APR-1998 (first entry)
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27-MAR-1996; AU-008965.
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WO9735971-A1.
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                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W36048;
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                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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This is the amino acid sequence of the cDNA clone Bc1-like (HAICH29), used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory alseases, various allergies, and as anti-infectious agents. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEDLVG 120
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21-DEC-1996; EDSB00.
12-JAN-1996; GB-000660.
[Purst P, Tatton WG, Waldmeier P;
WPI; 97-384980/35.
Pew isolated "Deprenyl" (RTM)-induced protein - used to develop products for use in the diagnosis and treatment of neural disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-NoV-1998 (first entry)
Amino acid sequence of the CDNA clone Bcl-like (HAICH29).
Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction; immunological disorder; autoimmune disease; anti-infectious agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Deprenyl" (RPM)-induced protein 1.
Deprenyl-induced protein; neuroactive drug; neural cell; apoptosis; neurodegenerative disorder; oligodendrocyte; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotides and encoded polypeptides - used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 75.1%; Score 1041; DB 1; Length 365; Best Local Similarity 96.5%; Pred. No. 1.22e-88; Matches 139; Conservative 5; Mismatches 0: Indels
                  121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA 168
QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA 168
                                                                                                                                                                                                                                                                                                                                            (AUCK-) AUCKLAND UNISERVICES LTD.
(HUMA-) HUMAN GENOME SCI INC.
Feng P, Gentz RL, Krissansen GW, Ni J, Rosen CA,
Su JY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 12A-12D; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 QVQEWMVAYLETRLADWIHSSGGW 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 QVQDWIVAYLETRLADWIHSSGGW 144
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                                                                                                                  ¥.
                                                                                                                  W59884 standard; Protein; 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                    21-JAN-1998; U00960.
21-JAN-1997; US-034205.
21-JAN-1997; US-034204.
                                                                                                                                                                                                                                                                                                                                                                                                                          98-414099/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; V41925
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                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                      23-JUL-1998
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                                                                                                                                    W59884:
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Disclosure; Page 37: 52pp; English.

The present sequence is described of a derivative of human Bcl-w
(see also Y05530), a pro-survival member of the Bcl-2 family that
is widely expressed and which is essential for spermatogenesis.

The invention relates generally to a method of treatment and to an immal model for the identification of molecules and genetic
animal model for the identification of molecules and genetic
animal model for the identification of infertility of male animals.

Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model
carries a mutation is at least one allele of the human or murine
bcl-w gene (see X25132-35) or in a gene associated with bcl-w.
Such animals have disorganised seminferous tubules and are
substantially infertile, but possess no other major abnormalities
as determined by histological examination. They can be used to
screen for therapeutic molecules including genetic sequences
capable of inducing, enhancing or otherwise facilitating
spermatogenesis in animals, or which can induce infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 QVQDWIVAXLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVAL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                    N-PSDB; X25134.
An animal model exhibiting reduced levels of a Bcl-w protein and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; T96577.

Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bcl-w; apoptósis; bcl-2; cell survival; treatment; therapy; cancer; diagnosis; degenerative disease.
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Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 193;
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Best Local Similarity 93.8%; Pred. No. 2.34e-117;
Matches 181; Conservative 9; Mismatches 2;
                                                                                                                                                                                                          16-SEP-1997; AU-009228.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Admus J. Cory S, Gibson L, Koentgen F, Print C;
WPI; 99-243890/20.
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Adams JM, Cory S, Gibson LM, Holmgreen SP; WPI; 97-489635/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                         protein associated with Bcl-w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-APR-1998 (first entry)
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27-MAR-1996; AU-008965.
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                                                                                                                                                                             16-SEP-1998; AU0764.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 AA;
                                                                                                 WO9913710-A1.
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WO9735971-A1.
                                       animal model.
                                                                            Homo sapiens.
                                                                                                                                         25-MAR-1999
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This sequence represents a novel human protein, bcl-w, encoded by the bcl-2 gene family and extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat bol-y protein; Rbol-y; human bol-y protein; Hbol-y; bol-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial Infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a mammalian bcy-1 protein.
The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y protein (Rbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein thought to be involved in programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, Alzheimer's Disease, neural and muscular degenerative diseases (especially multiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis- conditions where cells under go premature cell death as a result of triagers which may or may not be apparent. They may also be used in this way to develop cell lines which remain
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                                                                                                                                                                                                                                                                                                                                                              Indels 1; Gaps
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Novel bcl-y homologues of the rat and human bcl-2 protein - useful for modulating programmed cell death.

Claim 2; Columns 19-22; 26pp; English how-l protein.
                                                                                                                                                                                                                                                                                                                   Length 193;
                                                                                                                                                                                                                                                                                                                Score 1331; DB 1; L
Pred. No. 2.34e-117;
9; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W97394 standard; Protein; 192 AA.
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Best Local Similarity 93.8%;
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                                                                                                                                                                                                                                                                                                                                                            181; Conservative
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23-FEB-1995; US-012201.
11-FEB-1997; US-798897.
25-NOV-1997; US-978523.
(COCE-) COCENSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalian bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GALVTVGAFFASK 193
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                                                                                                                                                                                                                                                                       193 AA;
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                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   growth e.g. cancers the standard of the bol-2 family, components the mammalian bol-y protein is a member of the bol-2 family, components in the cell death pathway. The bol-2 family have both apoptotic activity and the apoptosis blocking activity bol-y falls in the apoptosis activity caregory. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired.
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                                                                                                                                                                                                                                                                                                                OVOEWMYAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
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                                                                                     Gaps
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                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human bcl-y protein.
bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1337; DB 1; Length 193;
Pred. No. 5.93e-118;
8; Mismatches 2; Indels
                                        Length 193;
                                                                                     Indels
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                                      Score 1337; DB 1; 1
Pred. No. 5.93e-118;
8; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W61392 standard; Protein; 193 AA.
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Best Local Similarity 94.3%;
Matches 182; Conservative
                                        y Match
Local Similarity 94.3%;
nes 182; Conservative
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23-FEB-1996; US-012201.
11-FEB-1997; US-798897.
(COCE-) COCENSYS INC.
Guactella J;
WPI; 98-446079/38.
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193 AA;
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US5789201-A.
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    Sednence
                                               Query Match
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                                                                                          Matches
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Novel bcl-y homologues of the rat and human bcl-2 protein - useful Novel bcl-y homologues of the rat and human bcl-2 protein - useful for modulating programmed cell death blastocaure; Columns 19-20; 26pp; English.

Disclosure; Columns 19-20; 26pp; English.

The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y protein (Rbcl-y) and Rbcl-y and Rbcl-y are homologues of the bcl-2 protein (Rbcl-y) and Shcl-y and Bbcl-y proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, Alzheimer's Disease, neural and muscular degenerative diseases (especially multiple sclerosis), myocardial camportophic lateral sclerosis-conditions where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain collines associated with prolonged cell life span such as cancer conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune contact.
                                                                                                                                           Protein sequence of the specification.
Protein sequence of large sequence of s
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Pred. No. 1.86e-117;
7; Mismatches 1; Indels
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T 8
W97393 standard; Protein; 192 AA.
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Local Similarity 95.3%;
Les 183; Conservative
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25-NOV-1997; US-978523.
(COCE-) COCENSYS INC.
Guastella J;
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23-FEB-1996; US-012201.
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US5883229-A.
16-MAR-1999.
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The mammalian bol-y protein is a member of the bol-2 family, components in the cell death pathway. The bol-2 family have both apoptotic activity and the apoptosis blocking activity. bol-y falls in the apoptosis activity category. The recombinent protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell
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Claim 2: Page 33: 52pp; English.

The present sequence is human Bcl.w, a pro-survival member of the present sequence is human Bcl.w, a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for Spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl.w gene (see X25132-35) or in a gene associated with bcl.w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 FSDLAAQLHVTPGSAQORFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 QVQDMIVAXLETRLADWIHSSGGWADFTALXGDGALEDARRLREGNWA-VSTVVTGAVAL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGGFAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                         Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-1999 (first entry)
Human Bcl-w protein essential for spermatogenesis.
Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.9%; Score 1343; DB 1; Length 193; 95.3%; Pred. No. 1.50e-118; ative 7; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 95.3%;
les 184; Conservative
                  11-FEB-1997; 798897.
23-FEB-1996; US-012201.
11-FEB-1997; US-798897.
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16-SEP-1998; AU0764.
16-SEP-1997; AU-009228.
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                                                                                      (COCE-) COCENSYS INC.
                                                                                                                                                                                                                    growth e.g. cancers
                                                                                                                                98-446079/38.
                                                                                                                                                    N-PSDB; V283333.
                                                                                                                                                                                                                                                                                                                                                                                                                       death is desired
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WO9913710-A1.
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  04-AUG-1998.
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                                                                                                      Guastella J
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Matches
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Novel bcl-y homologues of the rat and human bcl-2 protein - useful for modulating programmed cell death

Cor modulating programmed cell death

Claim 1: Columns 17-18: 26pp; English.

Cor modulating programmed cell death

Cor modulating programmed cell death

Cor modulating programmed cell death

Cor modulating benear bcl-y protein (Rbcl-y). The

Specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and

Cor Bbcl-y are homologues of the bcl-2 protein (Rbcl-y). Rbcl-y and

Cord honologues of treat conditions associated with a disruption of

Core cell death pathway. If they act as cell death withbitcors, they may be

Used in therapies to treat subjects suffering from: strokes, head trauma,

Cord in therapies to treat subjects suffering from: strokes, head trauma,

Alzhelmer's Disease, neural and muscular degenerative diseases

Core cell death, aging, spinal cord injuries and amyotrophic lateral

Coll death, aging, spinal cord injuries and amyotrophic lateral

Coll death, aging, spinal cord injuries and amyotrophic lateral

Coll death, aging, spinal cord injuries and amyotrophic lateral

Coll death, aging, spinal cord injuries and amyotrophic lateral

Coll death, aging, spinal cord injuries and amyotrophic lateral

Coll death, aging, spinal cord injuries and amyotrophic lateral

Coll death, aging, spinal cord injuries and amyotrophic lateral

Coll death of the spinal cord in contrast, if they act as cell death stimulators,

Coll death and auto/Apperimmune diseases. They may also be used to

Coll death in, and hence control, parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The human bol, yprotein.

The human bol, protein, Rhol-y, human bol-y protein; Hbol-y; bol-2 homologue; Bat bol-y protein; Rhol-y; human bol-y protein; Etoke; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
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                                                                                                                                                                                                                                                                                                                                                                                             61 FSDLAAQLHVIPGSAQQRFIQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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                                                                                                                                                                                                                       Indels 1; Gaps
                                                                                                                                                                                                                                                                    1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRT 60
other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including
                                                                                                                                                                                                                                                                                                                    1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.
                                                                                                                                                                            Length 193;
                                                                                                                                                                      Score 1341; DB 1; L
Pred. No. 2.38e-118;
8; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T 6
W97392 standard; Protein; 193 AA.
                                                                                                                                                                    Match 96.8%;
Local Similarity 94.8%;
les 183; Conservative
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23-FEB-1996; US-012201.
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                                                                                                                         193 AA;
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US5883229-A.
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                                                                                                                           Sequence
                                                                                                                                                                      Query Match
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N-PSDB; X15945
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                                                                                                                             Rattus sp.
US5883229-A.
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                                                                                                                                                                                                                                                                                                                                                                    protein associated with Bcl-w
Cliaim 2; Page 35; 52pp; English.
CC The present sequence is mouse Bcl-w, a pro-survival member of the English and Which is widely expressed and which is essential for The invention relates generally to a method of treatment and to an animal model for the identification of the extrament and to an animal model for the identification of fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating of infertility, or for reducing fertility, by modulating or spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene (see X25132-35) or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise in animals, or which can induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWAVSTVVTGAVALG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                 An animal model exhibiting reduced levels of a Bcl-w protein and/or
                                                                                                                                                                                                         Mouse Bcl-w protein essential for spermatogenesis.
Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1345; DB 1; Length 193; Pred. No. 9.52e-119;
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Adams J, Cory S, Gibson L, Koentgen F, Print C;
WPI; 99-243890/20.
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W97391 standard; Protein; 193 AA.
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Y05531 standard; Protein; 193 AA.
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95.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                    16-SEP-1998; AU0764.
16-SEP-1997; AU-009228.
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                                                                                          181 ALVTVGAFFASK 192
                                                                                                                   181 ALVTVGAFFASK 192
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                                                                                                                                                                                                                                                                                                                                                      N-PSDB; X25133
                                                                                                                                                                                                                                      animal model.
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Novel bcl.y handlogues of the rat and human bcl-2 protein - useful for modulating programmed cell death

For modulating programmed cell death

Protein modulating programmed cell death

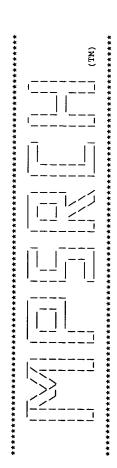
Protein conclusion also describes human bcl.y protein (Rbcl-y). The conclusion also describes human bcl.y protein (Rbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein thought to be involved in concern may be used to treat conditions associated with a disruption of programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y concerns may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, all concerns to bisease, neural and muscular degenerative diseases.

Concerns a bisease, neural and muscular degenerative diseases.

Concerns a program which may or may not be apparent. They may also be concerned beingers which may or may not be apparent. They may also be consequent to fringers which may or may not be apparent. They may also be consequent to treat conditions associated with this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, conditions and be apparent. They may be used to treat conditions associated with prolonged cell life span such as cancer (sepecially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites.
The rat bol-y protein.

The rat bol-y protein.

Rat bol-y protein, Rool-y; human bol-y protein; Hbol-y; bol-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple solerosis; myocardial infarction; vitally induced cell death; apping; empotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Raposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
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bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W61391 standard; Protein; 193 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-798897.
US-978523.
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25-NOV-1997; 978523.
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WPI; 99-214150/18.
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Fri Jun 23 14:17:41 2000; MasPar time 7.56 Seconds 601.720 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-155-327B-9 (1-192) from US09155327B.pep 1386 Description: Perfect Score: Sequence:

1 MPTPASTPDTRALVADFVGY......VTGAVALGALVTVGAFFASK 192

PAM 150 Gap 11 Scoring table:

188963 seqs, 23686106 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

1:genesedp a-geneseq36 Database:

Mean 32.566; Variance 139.419; scale 0.234 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| +[1000 |       | ap 2  |        |     |        |                          |           |
|--------|-------|-------|--------|-----|--------|--------------------------|-----------|
| No.    | Score | Match | Length | 80  | a      | Description              | Pred. No. |
| -1     | 1386  | 100.0 | 192    | Т   | Y05533 | Mouse Bcl-w protein de   | 8.04e-123 |
| 7      | 1345  | 97.0  | 193    | -   | X05531 | Mouse Bcl-w protein es   | 9.52e-119 |
| m      | 1343  | 96.9  | 193    | ٦   | W97391 |                          | 1.50e-118 |
| 4      | 1343  | 6.96  | 193    | -   | W61391 | Rat bcl-y protein.       | 1.50e-118 |
| S      | 1341  | 8.96  | 193    | -   | X05530 | Human Bcl-w protein es   | 2.38e-118 |
| 9      | 1337  | 96.5  | 193    | ٦   | W97392 | The human bcl-y protei   | 5.93e-118 |
| 7      | 1337  | 96.5  | 193    | ч   | W61392 | Human bcl-y protein.     | 5.93e-118 |
| 80     | 1332  | 96.1  | 192    | ,-1 | W97393 | Protein sequence of th   | 1.86e-117 |
| σι     | 1331  | 96.0  | 193    | ~   | Y05532 | Human Bcl-w protein es   | 2.34e-117 |
| 10     | 1331  | 96.0  | 193    | Н   | W36047 | Human bcl-w protein.     | 2.34e-117 |
| 11     | 1326  | 95.7  | 192    | Н   | W97394 | Mammalian bcl-y protei   | 7.33e-117 |
| 12     | 1235  | 89.1  | 168    | -   | W36048 | Mouse bcl-w protein.     | 7.82e-108 |
| 13     | 1041  | 75.1  | 365    | Н   | W59884 | Amino acid sequence of   | 1.22e-88  |
| 14     | 623   | 44.9  | 225    | -   | W19396 | "Deprenyl" (RTM) - induc | 1.06e-47  |
| 15     | 623   | 44.9  | 233    | -   | W31530 | Human anti-apoptotic B   | 1.06e-47  |
| 16     | 623   | 44.9  | 233    | Н   | R68887 | Human thymus BCL-XL.     | 1.06e-47  |
| 17     | 623   | 44.9  | 233    | Н   | W05821 | Bcl-XL protein.          | 1.06e-47  |
| 18     | 556   | 40.1  | 239    | -   | W87810 | A human Bcl-2 protein.   | 3.14e-41  |
| 19     | 545   | 39.3  | 239    | Н   | W87812 | A human Bcl-2-alpha pr   | 3.60e-40  |
| 20     | 545   | 39.3  | 239    | -   | R71404 | Human bcl-2 alpha prot   | 3.60e-40  |
| 21     | 545   | 39.3  | 239    | -   | R70331 | Human bcl-2 protein.     | 3.60e-40  |
| 22     | 545   | 39.3  | 239    | Н   | R42312 | Bcl-2 oncogene product   | 3.60e-40  |
| 23     | 545   | 39.3  | 239    | П   | W40217 | Human bc1-2.             | 3.60e-40  |

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Query Match 100.0%; Score 1386; DB 1; Length 192; Best Local Similarity 100.0%; Pred. No. 8.04e-123; Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps

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| 24 545 39.3 239 1 P80987 Sequence of bcl-2-alph 25 542 39.1 222 1 W01019 Apoptosis blocking pcc 25 542 39.1 222 1 W01019 Apoptosis blocking pcc 26 542 39.1 222 1 W01019 Apoptosis blocking pcc 29 542 39.1 222 1 W01018 Apoptosis blocking pcc 30 542 39.1 222 1 W01018 Apoptosis blocking pcc 30 542 39.1 229 1 W01018 Apoptosis blocking pcc 30 542 39.1 229 1 W01018 Apoptosis blocking pcc 32 23 38.6 222 1 W01018 Apoptosis blocking pcc 32 23 38.6 222 1 W01018 Apoptosis blocking pcc 32 23 38.6 222 1 W01018 Apoptosis blocking pcc 33 53 38.5 23 1 W0208 Human Bcl.2 munan bcl.2 | Sequence of bcl-2-alph 3 60e-40 Human oncogene bcl-2 p 3.60e-40 Apoptosis blocking pro 6.99e-40 A murine Bcl-2 mutant pro 6.99e-40 A murine Bcl-2 protein 6.99e-40 Human Bcl-2 wild-type 6.99e-40 Chicken lymphoid BcL-X 3.29e-39 Human Bcl-2 mutant pro 3.29e-39 Apoptosis blocking pro 3.29e-39 Human BcL-X gamma. 7.98e-39 Human BcL2. 5.13e-39 Human Bcl-2. A human Bcl-2. Sequence of bcl-2 protein 5.46e-35 Human bcl-2 beta prote 5.46e-35 Human bcl-2 pottein. 5.46e-35 Bcl-2 polypeptide. 5.46e-35 Sequence of bcl-2-beta Human Bcl-2 mutant pro 4.84e-28 Apoptosis-blocking pro 4.84e-28 Human thymus BCL-2. | ALIGNMENTS  dard; Protein; 192 AA.  (first entry)  protein deritvative.  lesis; Bcl-3; Bcl-2; mouse; fertility; infertility;  lesis; Bcl-3; Bcl-2; mouse; fertility; infertility;  LINST MEDICAL RES WALTER & ELIZA.  135.  135.  codel exhibiting reduced levels of a Bcl-w protein and/or sociated with Bcl-w  Page 39; 52pp; English.  Sequence is described of a derivative of mouse Bcl-w  135.  codel exhibiting reduced levels of a Bcl-w protein and/or sequence is described of a derivative of mouse Bcl-w  135.  codel exhibiting reduced levels of a Bcl-w protein and/or sequence is described of a derivative of mouse Bcl-w  135.  codel exhibiting reduced levels of a Bcl-w protein and/or sequence is described of a derivative of mouse Bcl-w  135.  codel exhibiting reduced levels of prematogenesis.  requence is deactification of molecules and genetic  ive lacks the 24 N-terminal amino acids of Bcl-w.  on relates generally to a method of treatment and to an  if for the identification of molecules and genetic  if for the identification of molecules and genetic  provided for the treatment of infertility, or for relation is at least one allele of the human or murine  (see X25132-35) or in a gene associated with bcl-w.  s have disorganised seminificatous tubules and are  (see X25132-35) or in a gene associated with bcl-w.  s have disorganised seminification. They can be used to therepout.  They can be used to the derivation of molecules including genetic sequences inducing, enhancing or which can induce infertility.  192 AA;   |
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| Ins  | 280987<br>4017344<br>4047344<br>4047346<br>4094346<br>401019<br>401018<br>401018<br>401018<br>401018<br>4010101<br>401021<br>401021<br>401021  | LIGNMEN LIGNMEN 12 AA. 14 AA. 15 mous 15 mous 16 MALTE Coentgen W W W W W W W W W W W W W W W W W W W  |
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| Ins  | 38888888888888888888888888888888888888   | protein<br>rst entr<br>sin deri<br>Bc1-3;<br>64.<br>664.<br>G1950.<br>30.<br>61950.<br>39, 52p<br>sice and vith<br>1, a pro<br>in  |
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| Ins  |  | 1<br>05533 st.<br>05533;<br>5-JUL-19<br>ouse BCl<br>permatcog<br>nimal sp.<br>09913719;<br>6-SEP-19;<br>6-SEP-19;<br>6-SEP-19;<br>6-SEP-19;<br>15-19;<br>15-19;<br>15-10sur<br>n animal x<br>n animal x<br>cotein as<br>see also<br>see also<br>sethods also<br>educing also<br>also also<br>educing |
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MYELOID CELL LEUKEMIA PROTEIN MCL-1 (FRAGMENT).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
                                                                                                                                                                                              58 DFHVESIDTARIIFNQVMEKEFEDGIINWGRIVTIFAFGGVL-LKKLPQEQIALDVGAYK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 -PNWGRLVAFFLFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTA 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 AGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGG 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEE R.M., GILLET G., BURNSIDE J., THOWAS S.J., NEIMAN P.; "Role of Nr13 in regulation of programmed cell death in the bursa of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
11.2%; Score 156; DB 13; Length 211;
Best Local Similarity 22.0%; Pred. No. 8.69e-10;
Matches 29; Conservative 32; Mismatches 70; Indels 1; Gaps
                                                                                                                            Score 162; DB 11; Length 172;
Pred. No. 8.16e-11;
20; Mismatches 31; Indels 7; Gaps
HATAKEYAMA S., HAMASAKI A., NEGISHI I., LOH D.Y., SENDO F., NAKAYAWA K., NAKAYAWA K.1.;
Int. Immunol. 0:0-0(1998).
EMBL; U23781; AAB97956.1; -.
EMBL; U23780; AAB97956.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SOFER L., BURNSIDE J.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF120210; AAD31644.1; -.
PROSITE; PS01080; BH1; 1.
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Last sequence update)
Last annotation update)
                                                          PROSITE; PS01080; BH1; 1.
PROMITE; PS01080; BH1; 1.
PFAM; PF00452; Bcl-2; 1.
SEQUENCE 172 AA; 20048 WW; 1B340DDD CRC32;
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SEQUENCE 211 AA; 23143 MW; DEE4E997 CRC32;
                                                                                                                                                                                                                                                                                                            211 AA.
                                                                                                                                                                                                                               117 QVSSFVAEFIMNNTGEWIRRNGGWED 142
                                                                                                                                                                                                                                              121 QVQEWMVAYLETRLVDWIHSSGGWAE 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fabricius.";
Genes Dev. 13:718-728(1999).
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                                                                                                                            Query Match
Best Local Similarity 32.6%;
Matches 28; Conservative
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Q9W6F1
Q9W6F1;
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077738
077738;
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                                                                                                                           BARTLING B., HOFFMANN J., HOLTZ J., SCHULZ R., HEUSCH G., DARMER D., "EXPression of apoptosis-associated genes in hibernating and stunned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 DPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 119; DB 4; Length 923;
Pred. No. 8.14e-04;
15; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 144; DB 6; Length 80;
Pred. No. 8.91e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 GDDINRRYDSEFQAMLQHLQPTAENAYEYFTKIASSLFESGINWGRVV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     myocardium of pig.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ001204; CAA04598.1; ...
HSSP: Q16611; IBXL.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases EMBL; AJ133769; CAB42643.1; ..
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor.
SEQUENCE 923 AA; 104203 MW; 1661174C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                               80 AA; 8818 MW; 973BE2D0 CRC32;
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Best Local Similarity 32.9%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Conservative
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                                                                                                   SEQUENCE FROM N.A.
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Sus scrofa (Pig).
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SEQUENCE
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09Y3R2
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BCL2A1D OR A1D.
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055179
055179;
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055177
055177;
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STRAIN-129/SVJ.

MEDLINE; 98336293.

CHAO J.R., WANG J.M., LEE S.F., PENG H.W., LIN Y.H., CHOU C.H.,

LI J.C., HUANG H.M., CHOU C.K., XEO M.L., XEN J.J.Y., VANG-YEN H.F.;

"mcl-1 is an immediate-early gene activated by the granulocyte-
macrophage colony-stimulating factor (GM-CSF) signaling pathway and is

one component of the GM-CSF viability response.";

""" rell. Biol. 18:4893-4898(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OKITA H., UMEZAWA A., SUZUKI A., HATA J.;

"Up-regulated expression of murine Mcll/EAT, a bcl-2 related gene, in
the early stage of differentiation of murine embryonal carcinoma cells
and embryonic stem cells."
Biochim. Biophys. Acta 1398:335-341(1998).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
::|::: :|:| |:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: ||:: |||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 167; DB 11; Length 331;
Pred. No. 1.11e-11;
30; Mismatches 64; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEG C.P., HSU S.Y., HSUEH A.J.W.; "Sequence of rat Mcl-1, a Bcl-2-related gene."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
                                                                                                                                                                                                                                                                                                         01-MAY-1997 (TrEMBLrel. 03, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
EAT/ACL-1 PROTEIN (MCL1).
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MGD; MGI:101769; MCI1.
PROSITE; PS01080; BH1; 1.
SEQUENCE 331 AA; 35217 MW; 3103C5FE CRC32;
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Q921P3 PRELIMINARY;
Q921P3 (921P4
01-MAY-1999 (TrEMBLED1. 10, C
01-MAY-1999 (TrEMBLED1. 10, L
01-NOV-1999 (TrEMBLED1. 12, L
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Local Similarity 25.2%;
hes 33; Conservative
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                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 YGDGALEEARR 161
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Р97287
Р97287;
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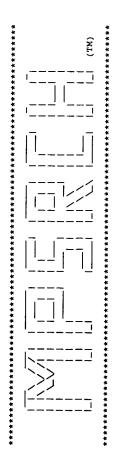
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 EIISRY-LREQATGSKDAKPLGEAGAAGRRALETLRRVGDGVQRNHETAFQGMLRKLDIK 218
                                                                                                                                                                                                                                                                                                                                         219 NEDDVKSFSRVMTHVFKDGVTNWGRIVTLISFGAFVAKHLKSINQESCIEPLAESITDVL 278
                                                                                                                                                                                                                                                                                                                                                                    6; Gaps
                                                                                                                                                                                                                                                                   16 DFVG-YKLRQKGYVC-GAGP-GE-GPAADPLHQAMRAAGDEFETRFRRFFSDLAAQLHVT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Gaps
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
B-CELL LEUKEMIA/LYMPHOMA 2 RELATED PROTEIN AlD (Al-D PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMPHOMA 2 RELATED PROTEIN AIB (A1-B PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-129/SV; TISSUB-LIVER;
HATAKEYAMA S., HAMASAKI A., NEGISHI I., LOH D.Y., SENDO F.,
NAKAYAMA K., NAKAYAMA K.-I.;
Int. Immunol. 0.0-0(1998).
ENBL; U23778; AAB97954.1; -.
ENBL; U23777; AAB97954.1; -.
ENBL; U23778; AB97954.1; JOINED.
MCD; MCI:1278326; BCl2alb.
PROSITE; PSO1080; BH1; 1.
PRAM; PFO0452; BCl-2; 1.
SEQUENCE 172 AA; 20048 MW; FA16DF6C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 163; DB 11; Length 172;
Pred. No. 5.48e-11;
20; Mismatches 31; Indels
                                                                                                                            Length 330;
                                                                                                                                                                                   Indels
                                                                                                                         Score 165; DB 11; 1
Pred. No. 2.47e-11;
33; Mismatches 75;
EMBL, AF115380; AAD13295.1; -.
HSSP; Q07817; IMAZ.
PROSTITE; PS01080; BH1; 1.
SEQUENCE 330 AA, 35195 MW; CC87F2E0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               279 VRTKRDWLVKQRGWDGFVEFFHVQDLEGGIR 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 QVSSFVAEFIINNTGEWIRRNGGWED 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 QVQEWMVAYLETRLVDWIHSSGGWAE 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match
Local Similarity 32.6%;
les 28; Conservative
                                                                                                                               y Match 11.8%;
Local Similarity 24.5%;
                                                                                                                                                                                   37; Conservative
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MEDLINE; 98024143.
HSU S.Y., KAIPIA A., MCGEE E., LOMELI M., HSUEH A.J.W.;
Bok is a pro-apoptotic Bcl-2 protein with restricted expression in reproductive tissues and heterodimerizes with selective anti-apoptotic Bcl-2 family members.";
Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 GDELE-QIRPSVYRNVARQLHIPLQSEPVVTDAFLAVAGHIFSAGITWGKVVSLYSVAAG 133
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INCHARA N., EKHTERAE D., GARCIA I., CARRIO R., MERINO J., MERRY A., CHEN S., NUNEZ G.;
SUBMITTER (DEC-197) to the EMBL/GenBank/DDBJ databases.
EMBL; AF027954: AAB87418.1;
EMBL; AF027707; AAC53582.1;
                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat), and Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                            Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 213;
                                                                                                                                                                       85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQDSFVDLY 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33; Mismatches 38; Indels
                                                                                                                                          8; Indels
                                                                                                                                                                                        HE X.J., JIN K.L., GRAHAM S.H., SIMON R.P.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR136230; AAD33683.1; -.
PROSITE; PS01259; BH.9; 1.
PROSITE; PS01260; BH4_1; 1.
SEQUENCE 170 AA; 19031 MW; 8B29C9C1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSU S.Y., HSUEH A.J.W.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY, TESTIS, UTERUS;
                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
BCL-2-RELATED OVARIAN KILLER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 LAVDCVRQAQPAMVHALVDCLGEFVRKTLATWLRRRGGWTD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 207; DB 11;
Pred. No. 6.91e-19;
11; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 175; DB 11;
Pred. No. 4.38e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23456 MW; 29761D17 CRC32;
                                                                                                                                                                                                                                                                  213 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 175;
                                                                                                                                                                                                                                                                PRT;
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                                                                                                               14.88;
                                                                                                                            Local Similarity 58.3%;
nes 28; Conservative
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Best Local Similarity 24.8%;
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Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00452; Bcl-2; SEQUENCE 213 AA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-MOUSE;
                                                                                                                                                                                                                                                                                                                                                           OR MTD.
                                                                                                             Query Match
                                                                                                                                                                                                                                                  LT 6
035425
035425;
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Q9W6F2;
                                                                                                                                          Matches
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TISSUE-OVARY, UTERUS;
HSU S.Y., HSUEH A.J.W.;
"A splicing variant of the Bcl-2 member Bok with a truncated BH3
domain induces apoptosis without dimerization with anti-apoptotic Bcl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSU S.Y., KAIPIA A., MCGEE E., LOMELI M., HSUEH A.J.; Bok is a pro-apoptotic Bcl-2 protein with restricted expression in reproductive tissues and heterodimerizes with selective anti-apoptotic Bcl-2 family members: ";
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                      87 GRIMTIFTFGGLL-TKKLQEHGVQLTGEEKE-KISYFITEYI--INNKAAWIDANGGWEN 142
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 99190706.
LEE R.M., GILLET G., BURNSIDE J., THOMAS S.J., NEIMAN P.;
"Role of Nr13 in regulation of programmed cell death in the bursa of
                                                                                                                                                                                                                                                                                                                                       27 GPAQTRVAHVLRNIASSLQDQTEEALRPFLDRIDITSVDVAKRIFNGVMEEKFADGNTNW 86
                                                                                                                                                                                                                                                                                                                                                          36 GPAADPLHQAMRAAGDEFETRFRTFSDLAAQLHVTPGSAQQR-FTQVSDELF-QGGPNW 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 SPTDKELVAQAKALGREYVHARLLRAGLSWSAPERASPAPGG-RLAEVCTVLLRLGITWG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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9
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                      DB 13; Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 11; Length 170;
                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                  SOFER L., BURNSIDE J.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF120211; AAD31645.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 proteins.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF051093; AAC61928.1; -.
SEQUENCE 170 AA; 18729 MW; 79B4BBE6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                      Pred. No. 3.32e-12;
46; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 22.3%; Pred. No. 4.97e-12; nes 25; Conservative 37; Mismatches 48
                                                                                                                                                                                                                          174 AA; 20095 MW; 70F5FDAA CRC32;
                                                                                                                                                                                                                                                                    12.2%; Score 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.1%; Score 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequ
NOV-1998 (TREMBLrel. 08, Last anno
BCL-2-RELATED OVARLAN KILLER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 GFLTKFERRSPLSFSTITDIFAAVLSL 169
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                                                                                                                                   Genes Dev. 13:718-728(1999).
                                                                                                                                                                                                                                                                                      Similarity 20.4%; 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=OVARY, UTERUS;
MEDLINE; 98024143.
                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                   Fabricius."
                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                      Query Match
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088857
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229 AA; 25099 MW; E82B3DFB CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
             SEQUENCE
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035843
035843;
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Q9WUI5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-B66/CBA; TISSUE-THYMUS;
MEDLINE; 98051053.
YANG X.-F., WEBER G.F., CANTOR H.;
"A novel Bcl-x isoform connected to the T cell receptor regulates apoptcosis in T cells.";
Immunity 7:629-639(1997).
EMBL; U51278; AAC53459.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 45.1%; Score 630; DB 11; Length 233; Local Similarity 53.8%; Pred. No. 1.97e-106; les 78; Conservative 30; Mismatches 35; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-HOLSTEIN; TISSUE-THYMUS;
REYES R.A., COCKERELL G.L.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
BCL2-LIKE (BCL-XL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:88139; BGI21.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01265; BH4_1; 1.
PFAM; PF00452; BG1-2; 1.
SEQUENCE 233 AA; 26033 MW; A4A14278 CRC32;
                                                                                                                                                                                          233 AA.
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                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::|| | | ::|
161 RLREG-N-WASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSTIE; PS01060; BH1; 1.
PROSTIE; PS01258; BH2; 1.
PROSTIE; PS01259; BH3; 1.
PROSTIE; PS01260; BH4_1; 1.
PFAM; PF00452; BC1-2; 1.
NON_TER 229 229
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                                                                                                                                                                                          PRELIMINARY;
                          181 GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCL-2 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovinae; Bos.
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002718
002718;
                                                                                                                                          LT 2
035844
035844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BCL2L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 AAGPAPSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARERFATVVEELFRD 130
                                                                                                                                                                                                                              131 GVNWGRIVAFFEFGGVMCVESVNREMSPLVDSIALWMTEYLNRHLHTWIQDNGGWDAFVE 190
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                               30 GAGPGEGPAADPLHQAMRAAGDEFETRFRRFFSDLAAQLHVTPGSAQQRFTQVSDELFQG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=B6/CBA; TISSUE=THYMUS;
MEDLINE; 9805103;
YANG X.-F., WEBER G.F., CANTOR H.;
"A novel Bcl-x isoform connected to the T cell receptor regulates apoptosis in T cells.";
mmunity 7:629-639(1997).
EMBL; U51277; AAC53458.1; -.
HSSP; P53563; IAF3.
                                                         5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 18.3%; Score 535; DB 11; Length 235; Local Similarity 59.0%; Pred. No. 6.46e-86; les 62; Conservative 24; Mismatches 19; Indels
   Length 229;
Query Match 42.2%; Score 590; DB 6; Length 229
Best Local Similarity 44.5%; Pred. No. 9.22e-98;
Matches 73; Conservative 46; Mismatches 40; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 LFGAALCAESVNKEMEPLVGQVQEWNVAYLETRLVDWIHSSGGWA 145
                                                                                                                                                                                                                                                                                                                                                                                       150 LYGDGALEEARRILREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                     191 LYGP-SM---RPLFDFSWLSLKALLSLAL-VGACITLGAYLGHK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26122 MW; FB0B0207 CRC32;
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STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGT:88139; Bc121.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01259; BH3; 1.
PFAM; PF00452; Bc1-2; 1.
SEQUENCE 235 AA; 26122 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Jun 23 14:15:12 2000; MasPar time 18.46 Seconds 724.726 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-155-327B-7 (1-193) from US09155327B.pep 1397 Description: Perfect Score:

1 MATPASAPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193 Sequence:

PAM 150 Gap 11 Scoring table:

225878 seqs, 69334122 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptremb112

1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human 5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle 5:sp\_hage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified 13:sp\_vertebrate 14:sp\_virus

Mean 44.702; Variance 83.297; scale 0.537 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

| Pred. No.                  | 5.72e-273 | 1.97e-106           | 9.22e-98          | 6.46e-86               | 6.91e-19     | 4.38e-13              | 3.32e-12    | 4.97e-12              | 1.11e-11               | 2.47e-11       | 5.48e-11               | 8.16e-11               | 8.69e-10              | 8.91e-08               | 8.14e-04               | 1.63e-03               | 1.72e-01         | 2.36e-01               | 2.36e-01        | 4.44e-01              |
|----------------------------|-----------|---------------------|-------------------|------------------------|--------------|-----------------------|-------------|-----------------------|------------------------|----------------|------------------------|------------------------|-----------------------|------------------------|------------------------|------------------------|------------------|------------------------|-----------------|-----------------------|
| Description                | BCL-W.    | BCL2-LIKE (BCL-XL). | BCL-2 (FRAGMENT). | BCL2-LIKE (BCL-X-GAMMA | BCL-X SHORT. | BCL-2-RELATED OVARIAN | PROTEIN A1. | BCL-2-RELATED OVARIAN | EAT/MCL-1 PROTEIN (MCL | MCL-1 PROTEIN. | B-CELL LEUKEMIA/LYMPHO | B-CELL LEUKEMIA/LYMPHO | MYELOID CELL LEUKEMIA | BAK PROTEIN (FRAGMENT) | NUCLEAR TRANSPORT RECE | B-CELL LEUKEMIA/LYMPHO | C42C1.4 PROTEIN. | HYPOTHETICAL 46.4 KD P | TRANSPORTIN-SR. | SIMILAR TO BCL-FAMILY |
| £1                         | 966880    | 035844              | 002718            | 035843                 | Q9WUI5       | 035425                | Q9W6F2      | 088857                | P97287                 | Q9Z1P3         | 055177                 | 055179                 | Q9W6F1                | 077738                 | Q9Y3R2                 | 055178                 | 044971           | 069657                 | Q9Y5L0          | 036423                |
| DB                         | =         | 11                  | 9                 | 11                     | 11           | 1                     | 13          | 11                    | 11                     | Ξ              | 11                     | 11                     | 13                    | 9                      | 4                      | 7                      | ស                | 7                      | 4               | 14                    |
| %<br>Query<br>Match Length | 193       | 233                 | 229               | 235                    | 170          | 213                   | 174         | 170                   | 331                    | 330            | 172                    | 172                    | 211                   | 80                     | 923                    | 128                    | 1259             | 451                    | 975             | 168                   |
| %<br>Query<br>Match        | 98.6      | 45.1                | 42.2              | 38.3                   | 14.8         | 12.5                  | 12.2        | 12.1                  | 12.0                   | 11.8           | 11.7                   | 11.6                   | 11.2                  | 10.3                   | 8.5                    | 8.4                    | 7.4              | 7.3                    | 7.3             | 7.2                   |
| Score                      | 1378      | 630                 | 290               | 535                    | 207          | 175                   | 170         | 169                   | 167                    | 165            | 163                    | 162                    | 156                   | 144                    | 119                    | 117                    | 103              | 102                    | 102             | 100                   |
| Result<br>No.              | -         | 7                   | m                 | 4                      | Ŋ            | 9                     | 7           | æ                     | σ                      | 10             | 11                     | 12                     | 13                    | 14                     | 15                     | 16                     | 17               | 18                     | 19              | 20                    |

181 GALVTVGAFFASK 193

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| 3.24e-01<br>4.44e-01<br>4.44e-01<br>6.07e-01<br>8.28e-01<br>1.53e-00<br>2.07e+00<br>2.07e+00<br>2.07e+00<br>2.07e+00<br>2.07e+00<br>3.78e+00<br>3.78e+00<br>3.78e+00<br>3.78e+00<br>3.78e+00<br>3.78e+00<br>3.78e+00<br>3.78e+00<br>3.78e+00<br>3.78e+00<br>3.78e+00<br>3.78e+00<br>3.78e+00  |
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### ALIGNMENTS

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| NARY; PRT; 193 AA.  rel. 08, Created)  rel. 08, Last sequence update)  rel. 12, Last annotation update)  Rat).  Chordata; Craniata; Vertebrata; Mammalia;  Chordata; Craniata; Vertebrata; Mammalia;  Sciurognathi; Muridae; Murinae; Rattus.  EX; TISSUE-BRAIN;  X., LINDHOLM D.;  Sciurognathi, Muridae; Murinae; Rattus.  Y., LINDHOLM D.;  Hari, I.  Hari, I.  Hari, I.  12. 1.  22. 1.  20820 MW; 6E5F84BA CRC32;  | h 98.6%; Score 1378; DB 11; Length 193;<br>Similarity 97.4%; Pred. No. 5.72e-273;<br>188; Conservative 4; Mismatches 1; Indels 0; Gaps | MATPASTPDTRALVADEVGYKLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60<br> | FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNNGRLVAFFVFGAALCAESVNKEMEPLVG 120<br> | QVQDWMVTYLETRLADMIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180<br>   :   :   : |  |
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| RESULT 1 1D 088996 AC 088996 O1 01-NOV-1 DT 01-NOT-1 D    | Query Match<br>Best Local<br>Matches 1   |   | 61   | 121  |  |
| RES<br>PTT DDT TTD DDT TT | OME  | Db<br>Qy  | Db<br>Qy   | Db<br>Qy   |  |

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#title Molecular analysis of mbcl-2: structure and expression of the murine gene homologous to the human gene involved in follicular lymphoma.
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##cross-references GB:M16506; NID:9468335; PIDN:AAA37281.1; PID:9387110
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                                                                                                                                                                                                                                                                                     #authors Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
#journal Nucleic Acids Res. (1992) 20:4187-4192

#title Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
neuronal organs in adult and embryo.
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transforming protein (bcl-2-beta) - human #formal_name Homo sapiens #common_name man 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 23-Feb-1997
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#length 199 #molecular-weight 22299 #checksum 7397
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28; Mismatches 31; Indels
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                                                                                                              ##residues 1-232 ##label CAZ ##cross-references EMBL:211961; NID:g62970 ##cross-references EMBL:211961; NID:g62970 FICATION #superfamily bcl transforming protein
#title Molecular cloning and DNA sequence analysis of cDNA encoding
   chicken homologue of the Bcl-2 oncoprotein.
#cross-references MUID:92379084
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#Journal J. Immunol. (1994) 153:4388-4398
#title Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
#cross-references MUID:95052604
                                                                                                                                                                                                                                                                                                            79 GCAAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTATGRFVAVVEELFRDGVNWV 138
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bcl-x transmembrane deleted - mouse
#formal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
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h-bcl-xbeta
#formal_name Homo sapiens #common_name man
21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change
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#length 214 #molecular-weight 23900 #checksum 9730
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                                                                                                                                                                                                                                    DB 2; Length 232;
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                                                                                                                                                                                                                                Score 567; DB 2; Length 232
Pred. No. 5.16e-88;
38; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Mismatches 21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTF 191
                                                                                                                                                                          mitochondrion; transmembrane protein
#length 232 #molecular-weight 25839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 SM---RPLFDFSWISLKTILS-LVLVGACITLGAYLGHK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #type complete
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##residues 1-214 ##label RES
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                                                                            preliminary
                                                                                                                                                                                                                        Query Match
Best Local Similarity 46.5%;
Marches 74; Conservative
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                                                                                                ##molecule_type mRNA
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Matches 63; Conser
                                                          S24390
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                                                 Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler,
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##cross-references GB:Z23110; GB:L20120; NID:9510898; PIDN:CAA80657.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.;
Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWVRTKPLVCPFSLASGQ 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #journal Cell (1993) 74:597-608
#title bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic cell death.
#cross-references MUID:93364977
#accession A47537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apoptosis regulator bol-x - chicken
#formal_name Gallus gallus #common_name chicken
03-May-1994 #sequence_revision 03-May-1994 #text_change
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                                                                                            Biochem. Biophys. Res. Commun. (1998) 248:147-152 Identification of a human cDNA encoding a novel bcl-x
                                                                                                                                                                                                                                                                                                                                                                                                              #molecular-weight 25290 #checksum 864
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                                                                                                                                                                                                                                  ##residues 1-227 ##label BAN
##cross-references GB:U72398; NID:g1622940; PIDN:AAB17354.1;
PID:g1622941
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#superfamily bcl transforming protein
#length 190 #molecular-weight 21467 #checksum
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#length 227 #molecular-weight 25290
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Pred. No. 6.90e-82;
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#accession JE0203
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Best Local Similarity 53.7%;
Matches 65; Conservative
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Best Local Similarity 59.8%;
Matches 67; Conservative
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JE0203
JE0203
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CLASSIFICATION #su
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Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L. Bndocrinology (1995) 136:232-241

Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 RDGVNWGRIVAFFEFGGVMCVGSVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #formal_name Rattus norvegicus #common_name Norway rat 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
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                                                                                                Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.
Gene (1994) 140:291-292
Cloning and sequencing of a cDNA encoding the rat Bcl-2
#formal_name Rattus norvegicus #common_name Norway rat
29-May-1998 #sequence_revision 29-May-1998 #text_change
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#length 233 #molecular-weight 26122 #checksum 8310
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#length 236 #molecular-weight 26550 #checksum 8001
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PID:g1004377
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Pred. No. 4.62e-90;
31; Mismatches 39; Indels
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41.4%; Score 579; DB 2; Length 236
Best Local Similarity 44.6%; Pred. No. 1.80e-90;
Matches 74; Conservative 43; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 VELYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
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#accession 167431
                                                                                                                                                                                         MUID: 94193015
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Best Local Similarity 50.3%;
Matches 73; Conservative
                                          16-Jul-1999
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ORGANISM
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Cell (1987) 49:455-463
Molecular analysis of mbcl-2: structure and expression of the
murine gene homologous to the human gene involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
#journal Nucleic Acids Res. (1992) 20:4187-4192

#title Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
neuronal organs in adult and embryo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 1.236 ##label NEG ##cross-references GB:L31532; GB:M16506; NID:9468336; PIDN:AAA37282.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87
                                                                                                                                                                                                                                                                            Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce,
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transforming protein bc1-2-alpha - mouse
#formal_name Mus musculus #common_name house mouse
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Biochim, Biophys. Acta (1992) 1132:109-113
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#accession A25960
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cell (1986) 47:19-28
Cloning and structural analysis of cDNAs for bcl-2 and a
hybrid bcl-2/immunoglobulin transcript resulting from the t
                                                                                                                                                                                                              Fa7332
Eguchi, Y.; Evert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. (1992) 20:4187-4192
Isolation and characterization of the chicken bcl-2 gene:
Expression in a variety of tissues including lymphoid and
neuronal organs in adult and embryo.
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#title Analysis of the structure, transcripts, and protein products of bcl-2, the gene involved in human follicular lymphoma.
#cross_references_MUID:86259760
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##residues_1-95,'A',97-109,'G',111-236,'S',238-239 ##label TSU
##cross-references GB:M13994; NID:q179366; PIDN:AAA51813.1; PID:q179367
##note this sequence has been corrected in reference A37332
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#journal BMBO J. (1988) 7:123-131

#title Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2--Ig fusion gene in lymphoma.

#cross-references MUID:88196071
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                                                                                  transforming protein bcl-2, splice form alpha - human #formal_name Homo sapiens #common_name man 31-Dec-1988 #sequence_revision 07-Jun-1996 #text_change 18-Jun-1996
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this report is a correction
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#accession A24426
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blocks apoptosis in hematopoietic cells
#superfamily bcl transforming protein
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proto-oncogene; transforming protein; transmembrane protein
#length 239 #molecular-weight 26266 #checksum 8323
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#journal Endocrinology (1995) 136:232-241
#title Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong #cross-references WIID:95129487
#accession 167432
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#formal_name Rattus norvegicus #common_name Norway rat
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Pred. No. 6.59e-92;
44; Mismatches 41; Indels
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#journal J. Immunol. (1994) 153:4388-4398
#title Cloning and molecular characterization of mouse bcl-x in and T lymphocytes.
#cross-references WUID:95052604
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#length 233 #molecular-weight 26130 #checksum 6378
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PID:g607177
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#journal Nucleic Acids Res. (1992) 20:4187-4192
#title Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
neuronal organs in adult and embryo.
#cross-references MUID:92375724
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mitochondrion; transforming protein; transmembrane protein
#length 233 #molecular-weight 25687 #checksum 99
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                                                         #authors Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M. #submission submitted to the EMBL Data Library, November 1994 #description IL-5 inhibits anti-IgM-induced apoptosis in an immature cell line through inductin of bcl-X1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transforming protein (bcl-2-alpha) - chicken #formal_name Gallus gallus #common_name chicken 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                #checksum 5739
                                                                                                                                                                                                                                                                        ##cross_references EMBL:X83574; NID:9695622; PIDN:CAA58557.1; PID:9695623
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                                  ##cross-references EMBL:U10101; NID:9506647; PIDN:AAA82173.1;
PID:9506648
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                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 44.0%; Score 615; DB 2; Length 233
Best Local Similarity 53.1%; Pred. No. 7.19e-98;
Matches 77; Conservative 30; Mismatches 36; Indels
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                                                                                                                                                                                                                                                                                                                         #superfamily bcl transforming protein
#length 233 #molecular-weight 26132
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Best Local Similarity 46.6%;
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##molecule_type mRNA
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Jun 23 14:14:03 2000; MasPar time 12.24 Seconds 743.766 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-155-327B-7 (1-193) from USO9155327B.pep 1397 Description: Perfect Score:

1 MATPASAPDTRALVADFVGY......LTGAVALGALVTVGAFFASK 193 Sequence:

PAM 150 Gap 11 Scoring table:

142080 segs, 47172406 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

pir63 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 45.096; Variance 88.441; scale 0.510 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Pred. No.                     | 4.47e-98                | 7.19e-98              | 7.19e-98             | 4.11e-92               | 6.59e-92 | 2.72e-91                | 1.80e-90               | 4.62e-90 | 4.89e-89  | 5.16e-88 | 4.13e-83                | 4.32e-82                | 5.90e-82                | 1,33e-76               | 3.39e-76 | 3.59e-74 | 3.59e-74 | 9.58e-55               | 7.46e-23                | 1.37e-21                | 1.37e-21                | 3.14e-21              | 1.75e-21                |  |
|-------------------------------|-------------------------|-----------------------|----------------------|------------------------|----------|-------------------------|------------------------|----------|-----------|----------|-------------------------|-------------------------|-------------------------|------------------------|----------|----------|----------|------------------------|-------------------------|-------------------------|-------------------------|-----------------------|-------------------------|--|
| Description                   | apoptosis requlator b 4 | BCL-X protein - rat 7 | bcl-x long - mouse 7 | transforming protein 4 |          | BCL-2 - rat (fragment 2 | qene bcl-2 protein - 1 |          | q protein | protein  | bcl-x transmembrane d 4 | apoptosis requlator b 4 | apoptosis requlator b 6 | transforming protein 1 |          |          | protein  | gene bcl-2 protein - 9 | bcl-2-associated prot 7 | bcl-2-associated prot 1 | bcl-2-associated prot 1 | Bak protein - human 3 | bcl-2-associated prot 4 |  |
| £                             | B47537                  | S51761                | 149056               | A37332                 | TVHUA1   | I67432                  | I53744                 | 167431   | TVMSA1    | S24390   | 149057                  | JE0203                  | A47537                  | D37332                 | TVMSB1   | TVHUB1   | B37332   | I58194                 | D47538                  | 138921                  | A47538                  | S58873                | 153295                  |  |
| BB :                          | 7                       | ~                     | 7                    | 7                      |          | ~                       | ~                      | ~        | Ч         | 7        | 7                       | ~                       | C3                      | N                      | -        | -        | ď        | ~                      | ~                       | N                       | ~                       | ~                     | 7                       |  |
| %<br>Query<br>Match Length DB | 233                     | 233                   | 233                  | 233                    | 239      | 236                     | 236                    | 233      | 236       | 232      | 214                     | 227                     | 190                     | 206                    | 199      | 202      | 216      | 154                    | 192                     | 143                     | 192                     | 211                   | 133                     |  |
| %<br>Query<br>Match           | 44.1                    | 44.0                  | 44.0                 | 42.0                   | 41.9     | 41.7                    | 41.4                   | 41.3     | 40.9      | 40.6     | 38.9                    | 38.5                    | 38.4                    | 36.6                   | 36.4     | 35.7     | 35.7     | 28.8                   | 16.8                    | 16.3                    | 16.3                    | 16.2                  | 16.1                    |  |
| Score                         | 616                     | 615                   | 615                  | 587                    | 586      | 583                     | 579                    | 577      | 572       | 267      | 543                     | 538                     | 537                     | 511                    | 509      | 499      | 499      | 402                    | 235                     | 228                     | 228                     | 226                   | 225                     |  |
| Result<br>No.                 | П                       | 7                     | m                    | 4                      | ស        | 9                       | 7                      | 80       | 6         | 10       | 11                      | 12                      | 13                      | 14                     | 15       | 16       | 17       | 18                     | 19                      | 20                      | 21                      | 22                    | 23                      |  |

| 4.75e-21<br>1.68e-120<br>1.68e-120<br>1.06e-13<br>1.06e-13<br>1.06e-13<br>1.06e-13<br>1.06e-13<br>1.06e-13<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1.06e-03<br>1 | 4.31e+00             | 3.25e+00<br>3.25e+00<br>3.25e+00                                      |
|---|----------------------|---|
| cdn-2 protein - human bcl-2-associated prot bcl-x short - mouse gene bcl-xshort prote NR-13 protein - quail hemopoletic-specific Bcl-2 related - human BCL2 homolog MCL1 - hapothetical protein hypothetical protein hypothetical protein probable alkaline pro conserved protein Ell?  ABC transporter sll17 angiotensine converting terminal oxidase (EC  | hypothetical protein | gag polyprotein hum<br>molybdopterin oxidore<br>alpha-2-macroglobulin |
| \$58875<br>149053<br>149053<br>167435<br>157473<br>139055<br>74776<br>74776<br>7703168<br>7703168<br>7703168<br>7703168<br>7703168<br>7703168<br>770318   | T08908-<br>H69002    | FOLJGG<br>H69271<br>A53102  |
| 0000000000000000  | 2 -                  | 1777  |
| 2111<br>2111<br>176<br>177<br>177<br>177<br>177<br>178<br>178<br>178<br>178<br>178<br>178   | 250                  | 522<br>896<br>4543  |
| 11111111111111111111111111111111111111  | 6.7                  | 6.7   |
| 225<br>218<br>2018<br>201<br>201<br>149<br>1150<br>1100<br>100<br>100<br>100<br>100<br>100<br>100<br>100<br>1   | 6 6<br>6 8           | 94<br>94<br>94  |
| 4 5 9 5 7 5 8 5 7 8 8 8 8 8 8 9 9 9 8 9 9 9 9 9 9 9 9 9   | 41                   | 44<br>44<br>5   |

## ALIGNMENTS

|     | NCE A47537 thors Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson, C.B. C.B. C.B. | cell<br>bcl-x<br>reg<br>erences M<br>B4753 | ##status nucleic acid sequence not shown; translated from GB/EMBL/DDBJ ##molecule_type mRNA # # # # # # # # # # # # # # # # # # # | status<br>molecule_<br>residues<br>cross-ref | ne GDB:BCL2L<br>##cross-references GDB:228079<br>FICATION #superfamily bc1 transforming protein<br>DS alternative splicing; apoptosis<br>E #product apoptosis requlator bc1-xL #status predicted | #label MAT\ 5,189-233 #product apoptosis regulator bcl-xS #status #label MA2 #length 233 #molecular-weight 26063 #checksum 5 | <pre>// Match 44.1%; Score 616; DB 2; Length 233; Local Similarity 53.1%; Pred. No. 4.47e-98; hes 77; Conservative 30; Mismatches 36; Indels 2; Gaps 2;</pre> |
|-----|---|--|---|--|--|--|---|
| O O | REFERENCE<br>#authors<br>#iournal   | #title<br>#cross-refe<br>#accession        | ##status<br>##molecu<br>##residu<br>##cross-  | ##status<br>##molecu<br>##residu<br>##cross- | #gene<br>##cross-<br>CLASSIFICATION<br>KEYWORDS<br>FEATURE<br>1-233  | 1-125,189-233<br>SUMMARY   | Query Match<br>Best Local S<br>Matches 7  |

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US 08/333,565

APPLICATION NUMBER:

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Job time : 12 secs.
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   85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
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                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 59, Application US/08661479
Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: NORSMEYER, Stanley J.
TITLE OF INVENTION: BC1-x/Bc1-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                           Length 233;
                                                                                                                                                                                                                                                                        / Match
44.1%; Score 616; DB 1; Length 233
Local Similarity 53.1%; Pred. No. 6.27e-44;
les 77; Conservative 30; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,448
FILING DATE: 19930622
                                                                                          ATTORNEY/AGENT INFO 423.

ATTORNEY/AGENT INFO 423.

NAME: No. 5646008thrup, Thomas E. REGISTRATION NUMBER: 33,268

REFERENCE/DOCKET NUMBER: ARCD90

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-744-0090

TELEFAX: 312-755-4489

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids

TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                       MOLECULE TYPE: protein
TENCE 233 AA; 26063 MW; 275311 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 59, Application US/08661479
                                                                                                                                                                                                                                                                                                                                                                                                                    205 KGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                              linear
                                                                        FILING DATE: 19
CLASSIFICATION:
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US-08-661-479-59
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85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                        Length 233;
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44.1%; Score 616; DB 2; Length 233
Local Similarity 53.1%; Pred. No. 6.27e-44;
les 77; Conservative 30; Mismatches 36; Indels
                                                                                               15726A-000700
                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECCLE TYPE: peptide
JENCE 233 AA; 26049 MW; 275801 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: Fri Jun 23 14:16:17 2000
FILING DATE: 31-OCT-1994
ATTORNEY AGENT INFORMATION:
NAME: Smith, William M. ACTSTRATION NUMBER: 30,223
REFERENCE/DOOKET NUMBER: 15726
TELECOMMUNICATION: TELECHONE: (415, 326-2420
INFORMATION: CASE OF SEQUENCE CHARACTERISTICS:
ENGUREE CHARACTERISTICS:
LENGTH: 233 amino acids
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ADDRESSEE: Townsend and Townsend Khourie and Crew
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US-08-081-448-6
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        TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF CORRESPONDENCE: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                     2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 59, Application US/08333565
Patent No. 5622852
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl.x/Bcl.2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
                                                                                                                                                                                                                                                                                                                                                                 Score 616; DB 3; Length 233;
Pred. No. 6.27e-44;
30; Mismatches 36; Indels
                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 AA.
                                                                                                                                                                                                                                              23647-20007.20
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                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
CE 233 AA; 26049 MW; 275801 CN;
                                             E: MORRISON & FOERSTER
755 Page Mill Road
                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 2364
TELECOMUNICATION INFORMATION:
TELEFONE: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 antho acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 59, Application US/08333565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 KGQERFNRWFLTGMTVAGVVLLGSL 229
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APPLICANT: BARR, PHILIP J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 53.1%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                              CITY: Palo Altó
STATE: California
COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                    FILING DATE:
                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-333-565-59
                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 616; DB 1; Length 233;
Pred. No. 6.27e-44;
30; Mismatches 36; Indels 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 321 No. 5646008th Clark Street, Suite 800 STATE: 1L COUNTRY: USA
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Patent No. 5646008
GENERAL INFORMATION:
APPLICANT: Thompson, Craig B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
JENCE 233 AA; 26049 MW; 275801 CN;
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                               379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Local Similarity 53.1%;
nes 77; Conservative
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COMPUTER READABLE FORM:
STREET: 3/> ___
CITY: Palo Alto
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Sequence 7, Application US/08470670A Patent No. 5834309
Patent No. 5834309 5710045
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Patent No. 6015687
GENERAL INFORMATION:
APPLICANT: KIEFER, MICHAEL C.
                                                                                                                                                                                                                                                                                                                                  233 amino acids
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Local Similarity 53.1%;
es 77; Conservative
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                                                                                                  STATE: Text
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 616; DB 4; Length 233;
Pred. No. 6.27e-44;
30; Mismatches 36; Indels
                                                                                                  Vertebrate Apoptosis Gene:
Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 AA.
   233 AA
                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                          TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TYPE: linear
MOLECULE TYPE: protein
SEQUENCE 233 AA; 26049 MW; 275801 CN;
                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US94/07089 FILING DATE: CONCURRENTLY FILED
                                                                                              TITLE OF INVENTION: Vertebrate Apop
TITLE OF INVENTION: Compositions and
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                       COUNTRY: United States of America ZIP: 77210
                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/081.448
FILING DATE: 22 JUNE 1993
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVIG L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD090
TELECOMMUNICATION INFORMATION:
TELECHOMOR: 512-320-7200
TELEFAX: 713-789-2679
   PRT;
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                                                                      Sequence 7, Application PC/TUS9407089 GENERAL INFORMATION:
APPLICANT:
                                                       Sequence 7, Application PC/TUS9407089
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Best Local Similarity 53.1%;
Matches 77; Conservative
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US-08-470-670A-7
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   PCT-US94-07089-7
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85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
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Pred. No. 6.27e-44;
30; Mismatches 36; Indels 2; Gaps
                                                                                                                                                                                                                                                                                                                                                         COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,670A
GENERAL INFORMATION:
APPLICANT: Thompson, Craig B. B.
APPLICANT: Bolse, Lawrence H.
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 AA.
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PTLING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD:090-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (512) 414-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                       NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
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SEQUENCE 233 AA; 26063 MW; 275311 CN;
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161 RLREG-N-WASVRTVLTGAVALGAL 183
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GENERAL INFORMATION:
                                       181 ALVTVGAFFASK 192
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COUNTRY:
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 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
            121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
                                                122 VQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181
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Patent No. 5789201
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL GUASTELLA JOHN
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYZHA: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.9%; Score 1367; DB 1; 1
97.4%; Pred. No. 1.95e-112;
ative 4; Mismatches 1;
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JENCE 192 AA; 20689 MW; 183185 CN;
                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/COCKET NUMBER: 1483
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                             Sequence 5, Application US/08798897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 192 amino acids
                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                           ZIP: 20005
COMPUTER READABLE FORM:
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tes 187; Conservative
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                                                                           181 ALVTVGAFFASK 192
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                        122 VQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION
TITLE OF INVENTION: Interaction of Proteins Involved in
TITLE OF INVENTION: a Cell beath Pathway
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 616; DB 4; Length 233;
Pred. No. 6.27e-44;
30; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Imbra, Richard J.
REGISTRATION NUMBER: 37,643
REFERENCE,DOCKET NUMBER: FP-LJ 1361
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: PCT/US95/04600
12-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application PC/TUS9504600
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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Matches 77; Conservative
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California
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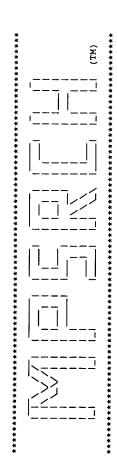
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1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF
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Pred. No. 1.58e-112;
                                                                                                                                                                                                                                                                       PARENTAL MESTALIA, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
GORRESPONDENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSE: STRNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: Washington
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM YAPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                    192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1483.0140001
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
TENCE 192 AA; 20701 MW; 181510 CN;
                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                              Sequence 6, Application US/08798897 Patent No. 5789201 GENERAL INFORMATION:
                                                                                                                                                                                                                            Sequence 6, Application US/08798897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-260
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,8
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 98.4%;
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                                                                                                               181 ALVTVGAFFASK 192
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121 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
                                                                                                          1 ATPASTPDTRALVADEVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
                         0; Gaps
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Pred. No. 1.95e-112;
4; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: Pebruary 11, 1997
CLASSIFICATION: 424
ATTONNEY/AGENT INFORMATION:
NAME: ESEMONA, ROBERT WITHOUS REFERENCE/DOCKET NUMBER: 32,893
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 32,893
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 117-2640
TELEFRAX: 202-371-2640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICAMT Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF SEQUENCES: 53
CORRESPONDENCE 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                           192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
JENCE 192 AA; 20689 MW; 183185 CN;
                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08978523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 97.9%;
Best Local Similarity 97.4%;
Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
STATE: DC
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                                                                                                                                                                                                                                                                                                              US-08-978-523-5
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61 FSDLAAQLHVTPGSAQORFTQVSDELFQGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                           121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
               1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 192;
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                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: herewith
CLASSIFICATION: 424
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Pred. No. 1.58e-112;
1; Mismatches 2;
                                                                                                                                                                                                         192 AA.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
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192 AA; 20701 MW; 181510 CN;
                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08978523
Patent No. 5883229
                                                                                                                                                                                                                                                                       Sequence 6, Application US/08978523
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                                                                                                                                                                                                                                                                                                      Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 6:
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NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 192 amino acids
amino acid
                                                                                                                                                                                                         STANDARD;
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                                                                                                                                      181 GALVTVGAFFASK 193
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Best Local Similarity
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                                                        61 FSDLAAQLHVTPGSAQORFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVVKEMEPLVG 120
Gaps
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                                                                                                                                                                                                                                                                                                                         APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SOUTENES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                      193 AA.
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FILING DATE: herewith
CLASSIFRCATION: 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFRCATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ES
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193 AA; 20820 MW; 185063 CN;
                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      Sequence 3, Application US/08978523
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
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Matches 188; Conservative
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                                                                                                                        121 QVQEWMYAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                          1 MATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                           Gaps
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TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
Length 193;
Score 1379; DB 1; Length 193
Pred. No. 1.54e-113;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDION TIPE: FIOPY GISH
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAMER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: Pebruary 11, 1997
CLASSIFICATION: 424
ATONEX/AGENT INPORMATION:
NAME: ESSONG, Robert W:
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 32,893
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                  193 AA.
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MOLECULE TYPE: protein
SEQUENCE 193 AA; 20832 MW; 183365 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08978523
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TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: not relevant
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                   STANDARD;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
Query Match 98.7%;
Best Local Similarity 98.4%;
Matches 190; Conservative
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STATE: DC
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                                                            Gaps
                                              1 MATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGGGPAADPLHQAMRAAGDEFETRFRRT 60
                       Gaps
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 Length 193;
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Mashington
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILIG DATE: February 11, 1997
CLASSIFICATION: 435
Score 1379; DB 2; I
Pred. No. 1.54e-113;
                                                                                                                                                                                                                                                                      193 AA.
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                        1; Mismatches
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MOLECULE TYPE: protein
JENCE 193 AA; 20820 MW; 185063 CN;
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Patent No. 5789201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483
TELECHOMINICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2600
                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08798897
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TYPE: amino acid
STRANDEDNESS: not relevant
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 97.4%;
Matches 188; Conservative
 Query Match 98.7%;
Best Local Similarity 98.4%;
Matches 190; Conservative
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STATE:
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protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Jun 23 14:16:05 2000; MasPar time 5.04 Seconds 552.912 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-155-327B-7 (1-193) from US09155327B.pep 1397 Description: Perfect Score:

1 MATPASAPDTRALVADFVGY..........LTGAVALGALVTVGAFFASK 193

Sequence:

PAM 150 Gap 11 Scoring table:

145341 seqs, 14437480 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5A\_COMB 2:5B\_COMB 3:6\_COMB 4:PCT\_COMB 5:backfiles1 Database:

Mean 30.708; Variance 142.172; scale 0.216 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Pred. No.                     | 1.54e-113  | 1.54e-113  | 1.90e-113  | 1.90e-113  | 1.58e-112  | 1.58e-112  | 1.95e-112  | 1.95e-112  | 6.27e-44   | 2.51e-41   | 2.51e-41   | 3.09e-41   | 3.09e-41   | 3.09e-41   | 3.09e-41   |
|-------------------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
|                               | Applicatio | Applicati  | Applicatio | Applicatio | Applicati  |            | Applicatio | Applicati  |            | Applicati  |
| u c                           |            |            | Α,         | <u>,</u>   |            |            |            | .,         | 2,4        | `.`        |            | 14,        | 59,        |            | <u>,</u>   | 14,        | 7,         | 3,         | 33         | o,         | 9          | o,         | 10,        |
| Description                   | Seguence   | Sequence   | ٠.         | Sequence   | Sequence   |            |            | Sequence   | Sequence   | Sequence   | Sequence   | Sequence   | Sequence   | Sequence 1 | Sequence 1 | Sequence 1 | Sequence   |
| ΩI                            | us-08-798- | us-08-978- | us-08-798- | us-08-978- | US-08-978- | ns-08-198- | US-08-978- | us-08-198- | PCT-US95-0 | PCT-US94-0 | US-08-470- | US-08-471- | US-08-333- | US-08-081- | US-08-661- | US-08-471- | US-08-607- | ns-08-607- | PCT-US95-0 | US-08-337- | ns-08-856- | US-08-248- | US-08-856- |
| DB                            | -          | 7          | -          | 7          | N          | Н          | ~          | Н          | 4          | 4          | ~          | m          | -          | Н          | 7          | Н          |            | -          | 4          | 7          | ~          | -          | 7          |
| %<br>Query<br>Match Length DB | 193        | 193        | 193        | 193        | 192        | 192        | 192        | 192        | 233        | 233        | 233        | 233        | 233        | 233        | 233        | 233        | 233        | 233        | 233        | 239        | 239        | 239        | 239        |
| &<br>Query<br>Match           | 98.7       | 98.7       | 98.6       | 98.6       | 97.9       | 97.9       | 97.9       | 97.9       | 44.1       | 44.1       | 44.1       | 44.1       | 44.1       | 44.1       | 44.1       | 44.1       | 44.1       | 42.0       | 42.0       | 41.9       | 41.9       | 41.9       | 41.9       |
| Score                         | 1379       | 1379       | 1378       | 1378       | 1368       | 1368       | 1367       | 1367       | 616        | 616        | 616        | 616        | 616        | 616        | 919        | 616        | 616        | 587        | 587        | 586        | 586        | 586        | 286        |
| Result<br>No.                 | ٦          | 7          | m          | 4          | 2          | 9          | 7          | 80         | σ          | 10         | 11         | 12         | 13         | 14         | 15         | 16         | 17         | 18         | 19         | 20         | 21         | 22         | 23         |

| 24 586 41.9 239 1 US-08-112- Sequence 10, Applicati 3.09e-41 25 584 41.8 236 1 US-08-607- Sequence 22, Applicati 4.67e-41 28 41.8 236 4 PCT-085-0 Sequence 20, Applicati 4.67e-41 28 581 41.6 239 3 US-08-607- Sequence 20, Applicati 8.68e-41 30 581 41.6 239 4 PCT-085-0 Sequence 21, Applicati 8.68e-41 21 41.6 239 4 PCT-085-0 Sequence 21, Applicati 8.68e-41 15.79 41.4 236 1 US-08-607- Sequence 21, Applicati 1.31e-40 25 41.2 239 1 US-08-607- Sequence 21, Applicati 1.31e-40 25 41.2 239 1 US-08-61- Sequence 21, Applicati 1.31e-40 25 41.2 239 2 US-08-61- Sequence 21, Applicati 2.99e-40 25 41.2 239 2 US-08-61- Sequence 21, Applicati 2.99e-40 25 41.2 239 2 US-08-61- Sequence 21, Applicati 2.99e-40 25 41.2 239 2 US-08-61- Sequence 21, Applicati 2.99e-40 25 41.2 239 3 US-08-113- Sequence 21, Applicati 2.99e-40 25 41.2 239 3 US-08-13- Sequence 21, Applicati 2.99e-40 25 41.2 239 3 US-08-13- Sequence 21, Applicati 2.99e-40 25 41.2 239 3 US-08-08- Sequence 21, Applicati 2.99e-40 25 41.2 239 3 US-08-08- Sequence 21, Applicati 2.99e-40 25 41.2 239 3 US-08-08- Sequence 21, Applicati 2.99e-40 25 41.2 239 3 US-08-08- Sequence 21, Applicati 2.99e-40 25 41.2 239 3 US-08-08- Sequence 21, Applicati 2.99e-40 25 41.2 239 3 US-08-08- Sequence 21, Applicati 2.99e-40 25 41.2 239 3 US-08-08- Sequence 21, Applicati 2.99e-40 25 41.2 239 3 US-08-28- Sequence 21, Applicati 2.99e-40 25 41.2 239 3 US-08-28- Sequence 21, Applicati 2.99e-40 25 41.2 239 2 US-08-28- Sequence 21, Applicati 2.99e-40 25 41.2 239 2 US-08-28- Sequence 21, Applicati 2.99e-40 25 25 41.2 239 2 US-08-28- Sequence 21, Applicati 2.99e-40 25 25 2 US-08-337- Sequence 15, Applicati 2.99e-40 25 25 2 US-08-240 25 2 US-08-240 25 2 US-0 | ALIGNMENTS  ID US-08-798-897-4 STANDARD; PRT; 193 AA.  XX  XX  XX  XX  XX  XX  XX  XX  XX | Sequence 4, Application US/08798897  Sequence 4, Application US/08798897  Sequence 4, Application US/08798897  Sequence 4, Application US/08798897  GENERAL INFORMATION:  APPLICANT: Guastella, John TITLE OF INVEWION: Genes Coding For Bcl-y, a Bcl-2  TITLE OF INVEWION: Homologue NUMBER OF SEQUENCES: 53  CORRESPONDENCE ADDRESS:  ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.C.  STREET: 1100 New YORK Avenue, N.W., Suite 600  CITY: Washington STATE: DC  COMPANE: DC  COMPANE: IBM PC Compatible  OPERATING SYSTEM: PC-DOS/MS-DOS  COMPUTER: Patentin Release #1.0, Version #1.30  CURRENT APPLICATION DATA:  CLASSIFCATION: WABER: US/08/798,897  FILING DATE: Petentin Release #1.0, Version #1.30  CLASSIFCATION: WORDER W.  RESPECTATION: WORDER W.  RESPECTATION: 1937  TELECOMMUNICATION HUMBER: 12,893  RESPECTATION WUMBER: 120.371-260  INFORMATION FOR SEQ ID NO: 4:  SEQUENCE CHARACTERISTICS:  LENGTH: 193 anno acids  TRELEVANT INFORMATION:  NOSCULE 193 AA; 20832 MM; 183365 CN; |
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Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:693460
                                                                                                                                                                                                                       211 accccaggetcagcccagcaacgettcacccaggtttccgacgaactttccaagggggc 270
                                                                                                                                                                                                                                                                                                             gtcaacaaagaaatggagcctttggtgggacaagtccaggattggatcgtggcctacctg 390
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                                                                                                                                                            231 GTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG 172
                                        gotgggcctggggaaggcccagccgccgccgctgcaccaagccatgcgggctgctgga 150
                                                                                                                                  151 gacgagititgagacccgiticcgccgcaccitcicigacciggccgctcagctacacgig 210
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                                                                                     470 GCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGGTCCACCTA-CCCTCCGCCAGGCCGGC 412
1; Gaps
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA939725 515 bp mRNA EST 01-MAY-199. vz92all.r1 Soares_thymus_2NbWT Mus musculus cDNA clone IMAGE:1344668 5' similar to gb:L31532_rnal Mouse bcl-2 gene encoding mbcl-2-beta (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
On Jan 19, 1998 this sequence version replaced gi:2285479.
Contact: Marna M/Mouse EST Project
WashIO-HHMX Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391 gagacacgtctggctgactggatccacagcagtggcggctggg 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 AACCGGCACCTGCACCTGGATCCAGGATAACGGAGGCTGGG 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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The WashU-HHMI Mouse EST Project
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/clone="IMAGE:1344668"
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/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J"
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Conservative
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Pred. No. 4.6e-17;
0; Mismatches 114; Indels 0;
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Best Local Similarity 60.6
Matches 175; Conservative
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4, 2000, 01:06:10 Search completed: July Job time: 16529 sec

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ACCESSION
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KEYWORDS
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/Glone="10" "NIH_BMAP_M_S3.1"
/Glone="10" "NIH_BMAP_M_S3.1"
/dev_stage="27.32 days"
/lab_host="DH100 [life Technologies)"
/note="vector: pr773D-pac (Pharmacia) with a modified
polylinker; Site=1: Not I; Site=2: ECO R1; The
NIH_BMAP_M_S3.1 library is a subtracted library of a
series, ultimately derived from a mixture of individually
tagged normalized libraries from ten regions of the mouse
brain (cerbellum, brain stems, olfactory bulbs,
hypothalamus, cortex, amygdala, basal ganglia, pineal
gland, striatum, hipoccampus) after a series of
subtractions to reduce the representation of cDNAs from
which ESTs had already been generated in this
process: NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1) was constructed
as follows: PCRamplified CDNA inserts from NIH_BMAP_M_S3
clones from which 3' ESTS had been derived was used as a
driver in a hybridization with the NIH_BMAP_M_S2
in the form of single-stranded circles. The remaining
                                                                                                                                                                                                                                                  Fax: 301 443 1706
Fax: 301 443 1706
Fax: 301 443 9890
Email: mESTefmail..nih.gov
Oligo-dr track not found, Not I site shown in beginning of sequence
10 1is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
available by the means that is soon to be determined. When NIH
determines the means for distribution of the BMAP cDNA clones, this
record will be updated accordingly when that means is determined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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TAG_LIB-NIH_BMAP_M_S3.1
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 gggaaggcccagccgccgacccgctgcaccaagccatgcgggctgctggagacgagtttg 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 agacccgtttccgccgcaccttctctgacctggccgctcagctacacgtgaccccaggct 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 AACTGGGGTACCGGAGAGGGTTCAGTGATCTAACATCCCAGGCTTCACATAACCCCAGGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 cagcccagcaacgcttcacccaggtttccgacgaacttttccaagggggccctaactggg 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 GGGAGGTGATTCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGGCGAGGCGATGAGTTTG 272
                                                                                         On Jul 7, 1999 this sequence version replaced gi:5866278. Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                        Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                        JOURNAL
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TITLE
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T 3/1; double-stranded cDNA was ligated to ECO RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M-Falima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever, M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tg92c06.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116234 3' similar to gb:M13995 PROTEIN BCL-2-BETA (HUMAN);contains TAR1.t2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 471)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
281 gccgtcttgtggcattctttgtctttggggctgccctgtgtgctgagagtgtcaacaaag 340
                                                                                                                                                                                     341 aaatggagcctttggtgggacaagtccaggattggatcgtggcctacctggagacacgtc 400
                                                                                                                                                                                                                   151 GTCGCATCGTGGCCTTTTTCTCCTTTGGCGGGGCACTGTGCGTGGAAAGCGTAGACAAGG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-1999
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/clone_lib="NoT_CGAP_CLL1"
/tissue_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
On Apr 7, 1998 this sequence version replaced gi:3035272.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 110.2; DB 46; Length 471; Pred. No. 5.6e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MER22 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www-bio.llnl.gov/bbrp/image/image.html
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/db_xref="taxon:9606"
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High quality sequence stop: 445.
Location/Qualiflers
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Best Local Similarity
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/tissue_type="total brain"
/dev_stage="3 months old"
/dev_stage="3 months old"
/note="corgan: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo (dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
2 others
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UI-W-BH2.1-apn-b-04-0-UI 3', mRNA sequence.
AW124015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 AGCGTAGACAAGGAGATGCAGGTATTGGTGAGTNGGATCGCAGCTTAGATGGCCACTTAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 ggagacgagtttgagacccgtttccgccgcaccttctctgacctggccgctcagctacac 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 gtgaccccaggctcagcccagcaacgcttcacccaggtttccgacgaacttttccaaggg 267
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                            Genexpress_library_idt: C; Genexpress_sequence_idt: y3c-25b06
Insert Length: 1145 Std Error: 0.00
Seq primer: (-21)M13_universal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 ggccctaactggggccgtcttgtgggcattctttgtctttggggctgccctgtgtgctgag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 agtgtcaacaaagaaatggagcctttggtgggacaagtccaggattggatcgtggcctac
                                                                                        Humain
Cedex, FRANCE
             Sep 21, 1992 this sequence version replaced g1:276079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 114.4; DB 21; Length 299;
Pred. No. 4.2e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="normalized infant brain cDNA" /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 ctggagacacgtctggctgactggatccacagcagtggcggctggg 433
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                                                                                        Genethon Centre de recherche sur le Genome
1, rue de 1'Internationale, BP60 91002 EVRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 454)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="c-25b06"
                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 339.
                                                                                                                                                                                           Email: genexpress@genethon.fr
Single read.
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Best Local Similarity 62.2%;
Matches 178; Conservative
                                   Contact: Genethon
Genexpress-Genethon
                                                                                                                                            Tel: 33169472800
Fax: 33160778698
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UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dr track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-Y0) was constructed as follows: PCR amplified cDNA inserts from previous library clones from which 3' ESTS had been derived were used as a driver in a hybridization with the normalized whole-eye library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-Y0 library. This procedure has been previously described (BODA) and SOBALES.
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1 (bases 1 to 299)

Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Auffray,C., Pohrat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Rabaktchis,C. and Tessier,A.

IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gccgtcttgtgggcattctttgtctttggggctgccctgtgtgctgagagtgtcaacaaag 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 aaatggagcctttggtgggacaagtccaggattggatcgtggcctacctggagacacgtc 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F08773 299 bp mRNA EST 20-FEB-1995 HSC25B061 normalized infant brain cDNA Homo sapiens cDNA clone c.25b06, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 gggaaggcccagccgccgacccgctgcaccaagccatgcgggctgctggagacgagtttg 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 agacccgtttccgccgcaccttctctgacctggccgctcagctacacgtgaccccaggct 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cagoccagoaacgottcacccaggtttccgacgaacttttccaagggggccctaactggg 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 CAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTTCGGGATGGGGTAAACTGGG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383 GGGAGGTAATCCCCATGGCAGCAGTGAAGCAAGCGCTGAGAAGGTGGCGTGGCGATGAGTTTG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 AACTGCGGTACCGGAGGATTCAGTGATCTAACATCCCAGCTTCATATAACCCCAGGGA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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95277534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 116.2; DB 51;
Pred. No. 1.6e-19;
0; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 tggctgactggatccacagcagtggcggc 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 g
                                                                                                                                                                                                                                                                                                                                                                                                                                     TAG_LIB=UI-R-YO
TAG_TISSUE=Eye
TAG_SEQ=CATTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.0%;
ilarity 59.6%;
Conservative (
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22-OCT-1999

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DB 79; Length 584;
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/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                           0; Mismatches 109;
                   Score 118.2; DB 7
Pred. No. 5.8e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-Y0-acg-g-07-0-UI"
/clone_lib="UI-R-Y0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Research Genetics (www.resgen.com)
Seg primer: M13 Forward
POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
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                   20.3%;
62.3%;
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Bonaldo, M.F., Lennon
                                          Best Local Similarity 62.3
Matches 180; Conservative
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AI716839/c
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Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).
EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: poustka@mping-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKEZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKEZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 German Genome Project.

No s1 sequence available.

This clone is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERNANY; Email: clone@rzpd.de.
                                                                                                    61 GCCGGGATTCAGTGACCTGACATCCCAGCTCCACATCACCACCCAGGACAGCATATCAGA 120
                                                                                                                                                                                                                                                                                                                                                     241 TGGTGAGTCGGATCGCAGCTTGGATGGCCACCTACCTGAATGACCACCTAGG 300
113 ccgccgaccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttcc 172
                                                                              173 gccgcaccttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaac 232
                                                                                                                                                               getteacccaggtttccgacgacttttccaagggggccctaactggggccgtcttgtgg 292
                                                                                                                                                                                                      121 GCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGG 180
                                                                                                                                                                                                                                                cattotttgtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctt 352
                                                                                                                                                                                                                                                                                                                             353 tggtgggacaagtccaggattggatcgtggcctacctggagacacgtctggctgac-tgg 411
                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL134785 584 bp mRNA EST 29-DEC-1999 DKF2p547K2090_r1 547 (synonym: hfbrl) Homo sapiens cDNA clone DKF2p547K2090 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                    1 CCACNGGAGCAGTAAAGCAAGCGCTGAGGGAGGCAGGCGACGACTTTGAACTGCGGTACC
                                                                                                                                                                                                                                                                        /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
145 c 173 g 116 t 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
On Jul 7, 1999 this sequence version replaced gi:5866255.
Contact: Poustka A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department Lehrach
Max-Planck Institute for Molecular Genetics
Ihnestrasse 73, 14195 Berlin, Germany
Tel: +49-30-84131128
Fax: +49-30-84131128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="DKFZp547K2090"
/clone_lib="547 (synonym: hfbr1)"
/tissue_type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="fetal"
/lab_host="X1-2blue"
                                                                                                                                                                                                                                                                                                                                                                                                              412 atccacagcagtggcggctggg 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 ATCCAGGAGAACGCCGGCTGGG 322
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Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                 413 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTTCTCCTTCG 472
                                                                                                                                                                                                                                                                         248 ccgacgaacttttccaagggggccctaactggggccgtcttgtggcattctttgtctttg 307
                                                                            128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
                                                                                                                                                                                                                                     188 acctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccaggttt 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtcc 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          473 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCANGTATTGGTGAGTCCNGATC 532
                                                                                                                                                    293 AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGCGCATTCAGTG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UI-R-Y0-acg-g-07-0-01.s1 UI-R-Y0 Rattus norvegicus CDNA clone
UI-R-Y0-acg-g-07-0-UI 3', mRNA sequence.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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AFB Eckstein Medical Research Building Iowa City, IA 52242,
Tel: 319 335 8260
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On May 18, 1998 this sequence version replaced gi:3136946.
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High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA 701 Queen Anne Avenue North, Seattle, WA 98109, USA 701 Gl6-3687

Fax: (206) 616-3687

Email: jwallacedu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 638 row: M column: 4
Seg primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 455)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                  AQ401160 455 bp DNA GSS 13-MAR-1999
HS_5062_A2_G02_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=638 Col=4 Row=M, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
                                                                                                                                                                432 ggcggacttcacagctctatacggggacggggccctggaggacgcacggcgtctgcggga 491
                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                              13-MAR-1999
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
  DB 109; Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 124; DB 106; Length 455;
Pred. No. 1.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="Plate=638 Col=4 Row=M"
/clone_lib="RPCI-11 Human Male BAC Library"
                                         9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mahairas GG, Wallace JC, Hood L
Score 135.6; DB 10
Pred. No. 2.4e-24;
0; Mismatches 9;
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                                                                                                                                                                                                                                                                            181 AACTGTAGGGGCCTTGTTTGCTAGCAAGTG 410
                                                                                                                                                                                                                                                        552 aactgtaggggcctttttgctagcaagtg 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 455.
Location/Qualifiers
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88.7%;
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      23.3%;
94.0%;
        Query Match 23.3%
Best Local Similarity 94.0%
Matches 141; Conservative
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Indels

17;

0; Mismatches

Matches 133; Conservative

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Best Local Similarity

432 ggcggacttcacagctctatacggggacgggccctggaggacgcacggcgtctgcggga 491

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/Glone="IMAGE:208187"
/clone="IMAGE:208187"
/clone_lbb="Soares_fetal_lung_NDHL19W"
/dev_stage="lpg weeks"
/dev_stage="lpg weeks"
/dab_bost="DH108 (amptcillin resistant)"
/lab_bost="DH108 (amptcillin resistant)"
/lab_host="DH108 (amptcillin resistant)"
/clouble-stranded cona was pize selected, ligated to Eco RI double-stranded cona, digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHH19W."
                                                                                                                                                                                                                                                                                                                                                                                          za73d06.rl Soares_fetal_lung_NbHL19W Homo sapiens CDNA clone
IMAGE:298187 5' similar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob. REGARET
High quality sequence stop: 383.
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                                                                                gggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactgggggccctggt 551
Tobases 1 to 437)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Holman,M., Rikkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                    18-APR-1996
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:785898.
Contact: Wilson RK
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/organism="Homo sapiens"
                                                                                                                                                                                         552 aactgtaggggccttttttgctagcaagtg 581
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  BCL-X.; mRNA sequence.
W01420
W01420.1 GI:1273428
                                                                                                                                                                                                                                                                                                                                                                               437 bp
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                                                                                           492
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cDNA synthesis with oligo dT Xba I (Xba I cloning site). RNA: stage 50-56 tadpoles, total brain tissue, GTC extraction method."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          library availability, please contact Pieter de Jong (pleter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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1 (bases 1 to 628)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
Use of BAC Cand Sequences from Library RPCI-11 for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                 296 tctttgtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttgg 355
                                                                                                                                                                                                                                                                                                                                                                                          acagcagtggcggctgggcggacttcacagctctatacggggacggggccctggaggacg 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      476 cacggogtctgcggggaaggcaactgggcatgagtgagcacagtggtgacggggccgtgg 535
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Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                          18-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                   tgggacaagtccaggattggatcgtggcctacctggagacacgtctggctgactggatcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
On Feb 19, 1999 this sequence version replaced gi:4145213.
On Feb 19, 1999 this sequence version replaced gi:4145213.
Chter_GSS: RPCI-11-352LS.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                 25.8%; Score 150; DB 71; Length 416; 70.3%; Pred. No. 5.2e-28;
                                                                                                                                                                                                                        85; Indels
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                                                                                                                                                                                          Best Local Similarity 70.38 Matches 201; Conservative
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1. 628 /organism="Homo sapiens" /db\_xref="GDB:7635052" /db\_xref="taxon:9606" /clone="RPCI-11-35215"

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 549)
Mahairas, G.C., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
tr from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Blate: 916 row: B column: 11
Seq primer: T7
Class: BAC ends
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
                                                                                                                                                                                                                                                                                    AQ665088 549 bp DNA GSS 23-JUN-1999 HS_5340_B1_A06_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=916 Col=11 Row=B, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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8 t 10 others
                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                         DB 108; Length 628;
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/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                   23.9%; Score 138.8; DB 108; Length
95.3%; Pred. No. 3.9e-25;
Live 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBACe3.6;
126 c 190 g 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353 AACTGTAGGGGCCTTTTTTGCTAGCAAGTG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 552 aactgtaggggccttttttgctagcaagtg 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 549.
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                                                                                                                 237 g
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                                                                                                               130 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                 128 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99380589
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AQ665088
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/note="Vector: Lambda Zap I; Site_1: XbaI; This library was supplied by Holly Cline (Cold Spring Harbor Labs).
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Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Fax: 516 367 8884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="2s50h02"
/clone=lib="Xenopus EST library"
/tissue=type="total brain tissue"
/cell_line="W22-TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate: za50 row: h column: 02
Seq primer: M13 universal forward primer
High quality sequence stop: 416.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mccombie@cshl.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW159063.1 GI:6271092
                                                                                                                                                                                                                                                                                                                                                   Query Match 30.8%;
Best Local Similarity 98.4%;
Matches 181; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  African clawed frog.
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COMMENT
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KEYWORDS
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The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized corpus striatum library cDNA library Preparation: M.B. Soares Lab Clone distribution: HI BMAP CDNA clones will be made available by the means that is soon to be determined. When NIH ecord will be updated accordingly when that means is determined. Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="ful-wBH1=baxe=10-0-UI"
/clone="ful-wBH1=baxe=10-0-UI"
/clone=lib="NIH_BMAP_M_S2"
/dev_stage="27:32 days"
/dev_stage="27:32 days"
/lab_host="bH10B (Life Technologies)"
/lab_host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 431)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW048567 431 bp mRNA EST 18-SEP-1999 UI-M-BHIL-alx-e-10-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BH1-alx-e-10-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                       61 aggetgaggeagaagggttatgtetgtggagetggggeetgggggaaggeecageegeegae 120
                                                                                                                                           ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
                                                                                                                                                                                 334 TTCTCCGATCTGGCAGCTCAGCTGCATGTGACCCCGGGCTCGGCCCAGCAACGCTTCACC 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                         On Feb 18, 1999 this sequence version replaced gi:4297581.
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
7082-9643, USA
7el: 301 443 19890
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
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DEFINITION

ACCESSION VERSION KEYWORDS

AW048567/c

RESULT

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ORGANISM

SOURCE

REFERENCE AUTHORS

TITLE

JOURNAL MEDLINE COMMENT

source

FEATURES

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used for subtraction consisted of a pool of 5,000 clones from the NIH_BMAP_M_S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries.

TAG_LIB=NIH_BMAP_M_S2
TAG_TISSUE=corpus-striatum
a 131 c 85 g 110 t
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Schutz,K., de la Bastide,M., Huang,E.N., Nascimento,L., Preston,R.,
Schutz,K., Swaby,I., Shekher,M., Spiegel,L., Vil,M.D. and
McComble,W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW159063 416 bp mRNA EST 05-NOV-1999 2a50h02.xl Xenopus EST library Xenopus laevis cDNA clone 2a50h02
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Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 gacgaactttccaaggggccctaactggggccgtcttgtggcatctttgtctttggg 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             431 GACGAACTITICCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCAITCTTTGTCTTTGGG 372
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Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3189433.
Contact: W. Richard McCombie
                                                                                                                                                                                                                                                                                                           Score 179.2; DB 64; Length 431;
Pred. No. 2.4e-35;
0; Mismatches 3; Indels 0;
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EST discovery in cattle Unpublished (2000)
Unpublished (2000)
Un Dec 20, 1995 this sequence version replaced gi:1133576.
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Weat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Fax: 402 762 4360
Smail: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
VO.980904.e. Vector identified by cross_match with the -minscore 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Design and use of four pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                                                                                           gcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctc 185
                                                                                                                                                                                                                 269 TTCCGACGAACTTTTCCAAGGGGCCCTAACTGGGGCCCGTCTTGTGCATCTTTGTCTTTGTCTT 328
                                                  149 GCACCAAGCCATGCGTGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adream and andometrium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 433)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A. and
                                                                                                                                                                                         246 ttccgacgaacttttccaagggggccctaactgggggccgtcttgtggcattctttgtctt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20104 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                  306 tggggctgcctgtgtgctgagagtgtcaacaa 338
                                                                                                                                                                                                                                                                                                            329 TGGGGCTGCCCTGTGTGCTGAGAGTGTCACAAA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adrenal, and endometrium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORWARD: GTTTTCCAGTATCACGAGG
BACKWARD: GTTTTCCAGTACGAGG
Plate: 10 row: G column: 24
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="pooled"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                      Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 362)
Marray M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                              AA596919 362 bp mRNA EST 19-SEP-1997 vo21f08.rl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:1050567 5' similar to TR:E123735 E123735 Rl MRNA.;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
On Dec 18, 1996 this sequence version replaced gi:1734345.
Contact: Marra M/Mouse EST Project
WashIngton University School of MedicineP
H44 Prorest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
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Pred. No. 3e-71;
0; Mismatches 7; Indels 0;
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/cell_line="C2C12"
/lab_host="DH108"
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Location/Qualifiers
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/clone="IMAGE:1050567"
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Best Local Similarity 97.9%;
Matches 326; Conservative 0
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0; Gaps
DB 80; Length 433;
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| COMMENT On May 18, 1998 this sequence version replaced gi:3137956. | Contact: Marsa M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1810 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This Clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:1003678 Seq primer: custom primer used High quality sequence stop: 465. FEATURES Location/Qualifiers | <b>v</b>  | DRIGIN  DRIGIN  Query Match  Query Matches 420; Conservative 0; Mismatches 9; Indels 1; Gaps 1;  Qy 1 atgcogaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60 | Oy 121 ccgctgcaccaagccatgcgggctgctggagacgatttgagaccgttccgccgcacc 180  |
|--|--|---|--|---|
| Description  | AW258810 um74a02.y<br>AA596919 vo21f08.r<br>AW359610 10104 MAR<br>AW048567 UI-M-BHI-<br>AW159063 za50h02.x<br>AQ532175 RPCI-II-3<br>AQ65088 HS_5340_B<br>AQ401160 HS_5602_A<br>W01420 za73406.rI<br>AL134785 DKFZp547K<br>AI716839 UI-R-Y0-a   | F0873 HSC25B061 n AW124015 UT-M-BH2. AN1401297 tg92c06.x AA99725 v292a11.r AI140733 ubp1d09.r AA50973 vh52c06.r AA50973 vh52c06.r AA149300 Rattus no AW149803 ha15d05.x H09884 m05b07.r1 A1323048 m141h10.y AV138827 AV138827 AN13827 AV138827 AN13827 AN26990.r AN1520744 ubolh10.r AM458294 vg48603.r AM458294 vg48603.r AN153013 Drosoophil  | M42014 m<br>M42014 m<br>ALO693013<br>ALO6545<br>AW072826<br>AW355100<br>ALO5940<br>ALO59400<br>ALO59400<br>ALO59400<br>ALO59400  | AW258810 540 bp mRNA EST 23-DEC-1999 um74a02.y1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2300906 5' similar to SW:BCLW_MOUSE P70345 APOPTOSIS REGULATOR BCL-W. [2] SW:BCLW_MOUSE ;, mRNA sequence. AW258810.  AW258810.  GI:6631791  EST.  house mouse.  Mus musculus  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  Eukheria; Rodentia; Sciurognathi; Muridae; Mus.  I (bases 1 to 540)  Marra.M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,  To Assas 1 to 540)  Marra.M., Hillier,L., Schury, M., Pape,D., Harvey,N., Schurk,R.,  Futter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,  Waterston,R. and Wilson,R.  The WashU-NCI Mouse EST Project 1999   |
| Score Match Length DB ID   | 55.6<br>39.6<br>39.6<br>39.6<br>39.6<br>39.6<br>23.9<br>23.9<br>23.9<br>22.3<br>23.9<br>22.3<br>22.3<br>22.3   | 1114.4 19.7 299 21 F0873<br>1100.2 19.0 451 46 AIV12015<br>1106.6 18.3 515 40 AA99725<br>104 17.9 472 43 AII80733<br>96.6 18.6 471 34 AA509753<br>70.2 12.1 1696 83 AF149300<br>57.4 9.9 576 481 AAF18903<br>57.4 9.9 576 481 AAF18903<br>57.4 9.9 576 22 H09884<br>44.4 7.6 497 27 AA016399<br>44.2 7.6 497 27 AA01441<br>44.2 7.6 592 27 AA01441<br>44.2 7.6 592 27 AA01441<br>42.6 7.3 418 34 AA458294<br>42.2 7.3 418 34 AA458294<br>42.2 7.3 418 34 AA458294<br>41.6 7.2 534 44 A1322704 | 7.2 545 26<br>7.1 925 82<br>7.1 1446 27<br>7.0 1201 83<br>7.0 714 64<br>6.9 377 80<br>6.8 634 44<br>6.8 835 49<br>6.6 844 82<br>6.6 844 82<br>6.6 844 82   | RESULT 1  AW258810 540 bp mRNA EST 23-DEC-199  DEFINITION UM74002.y1 Sugano mouse kidney mkia Mus musculus CDNA clone IMAGE:2300906 5' similar to SW:BCLW_MOUSE P70345 APOPTOSIS  RECGILATOR BCL-W. [2] SW:BCLW_MOUSE ; mRNA sequence.  AW258810.1 GI:6631791  EST SOURCE.  MUS musculus  ENERGANISM Marzeulus  ENERTERNCE.  Mus musculus  EUkaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia  EUkaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia  EUkaryota; Metazoa; Chordata; Craniata; Wartinae; Mus.  EUkaryota; Marzeulus  EUkaryota; Marzeulus  EUkaryota; Marzeulus  EUkaryota; Mayaller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T  Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,  Underwood, S., Shaller, T., Gibbons, M., Pape, D., Harvey, N., Schur  RITTLE The WashD-NCI Mouse EST Project 1999  JOURNAL Unpublished (1999) |

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Query
Result
                                        July 4, 2000, 01:06:08; Search time 795.04 Seconds (without alignments) 2962.018 Million cell updates/sec
                                                                              1 atgccgaccccagcctcaac......gccttttttgctagcaagtg 581
                                                                                                                       9714632
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                            4857316 seqs, 2026611650 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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|  | <br> | <br> |  |

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Sequence 2, Application PC/TUS9306251
Sequence 2. Application PC/TUS9306251
GENERAL INFORMATION:
APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
NUMBER OF SEQUENCES: 93
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                                                                                                                                                                                                       Sequence 4, Application PC/TUS9305651
GENERAL INPORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.5%; Score 125; DB 6; Length 5086; 58.9%; Pred. No. 3.7e-26; tive 0; Mismatches 150; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: 1459..2178
; OTHER INFORMATION: /product= "Bcl-2"
PCT-US93-05651-4
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US93/05651
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 5086 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 58.9
Matches 215; Conservative
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                                                                                                       2062 TACGG 2066
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PCT-US93-06251-2
                                                                                                                                                                     RESULT 14
PCT-US93-05651-4
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2002 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG 2061
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Pred. No. 3.7e-26;
0; Mismatches 150; Indels
                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 19930630
CLASSIFICATION:
ATORNEY AGENT INFORMATION:
NAME: DIGIGILO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
                 ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: July 4, 2000, 01:24:30 Job time: 14818 sec
                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 516-742-4343
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Best Local Similarity 58.9%;
Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 5086 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
                                                                                                                                       ZIP: 11530
COMPUTER READABLE FORM:
CORRESPONDENCE ADDRESS:
                                                                                                                   USA
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                                                                                                                   COUNTRY:
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Pred. No. 3.7e-26;
0; Mismatches 150; Indels
COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPPRATIS: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
                                                                                                                                CLASSIFICATION: 0.1.
ATTOMES AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION UNDER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
TELECOMMUNICATION INFORMATION:
TELEFENCE, (415) 324-080
TELEFENCE, (415) 324-080
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 5086 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                            INDIVIDUAL ISOLATE: human bcl-2 cDNA
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58.9%;
                                                                                                                                                                                                                                                                                                                                                CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 58.9
Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         ) NAME/KEY: CDS
; LOCATION: 1459..2178
US-08-365-486A-14
                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CL
HYPOTHETICAL: NO
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1762 GACGACTICICCCGCCGCTACCGCGGCGACTICGCCGAGAIGICCAGCCAGCTGCACTG 1821
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                                                                                                                                      OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
APPLICANT: Reed, John TITLE OF INVENTION: Regulation of bcl-2 Gene Expression NUMBER OF SEQUENCES: 29 CORRESPONDENCE ADDRESS: ADDRESSEE: OBLON, SPIVAR MATERIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 150; Indels
                                                                                                                                                                                          STREET: 1755 S. Jefferson Davis Hwy., Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-001-1995
RIGHOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-5EP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: FORTHOW, Andrew D.
REGIETRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-
TELECOMMUNICATION INFORMATION:
TELEFAX: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 5086 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 22202
                                                                                                                                                                                                                  Arlington
                                                                                                                                                                                                                                                Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY:
US-09-080-285-19
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                                                                                                                                                                                                                                                                              Length 4825;
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                                                                                                                                                                                                                                                                                                                0; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Reed, John
TILLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SECRENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                            21.5%; Score 125; DB 7; 58.9%; Pred. No. 3.7e-26;
             APPLICATION NUMBER: US/08/228,704
FILING DATE: 18-APR-1994
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 994,941
FILING DATE: 23-DEC-1992
APPLICATION NUMBER: 663,010
FILING DATE: 19-MAR-1991
APPLICATION NUMBER: 883,687
FILING DATE: 09-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/08465485A Patent No. 5831066
                                                                                                                                                                                                                                                                                                              Matches 215; Conservative
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 05 CLASSIFICATION:
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                                                                                                                                                                              ; SEQ ID NO:1:
: LENGTH: 4825
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1822 ACGCCCTTCACCGCGCGGGACGCTTTGCCACGGTGGTGGAGGAGGACTCTTCAGGACGGG 1881
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US-08-365-486A-14

Sequence 14, Application US/08365486A

Sequence 14, Application US/08365486A

GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
ITILE OF INVENTION: Tissue Specific Hypoxia Regulated
ITILE OF INVENTION: Therapeutic Constructs
ITILE OF ENVENTION: Therapeutic Constructs
CORRESPONDENCE ADDRESS:
ADDRESSEE: Defilinger & Associates
STREET: 350 Cambridge Avenue, Suite 250

CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 21.5%; Score 125; DB 3; Length 50
Best Local Similarity 58.9%; Pred. No. 3.7e-26;
Matches 215; Conservative 0; Mismatches 150; Indels
                                                                                                                                FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0S 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: FOLIDBY, ANGTEW D.
REFERENCE/DOCKET NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 19:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 5086 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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2062 TACGG 2066
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US-08-465-485A-19
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Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Read
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
                                                                                                                                                                                                                                                                                                    21.5%; Score 125; DB 3; Length 71 58.9%; Pred. No. 1.8e-26; rative 0; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Alington STATE: U.S.A. Learners nay; Surce to STATE: Virginia COUNTRY: U.S.A. 2007TRY: U.S.A. 2202 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/080,285
TELECOMMUNICATION INFORMATION: TELEPHONE: (408) 436-2070
                               TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                         LENGTH: 717 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                      Query Match 21.59
Best Local Similarity 58.99
Matches 215; Conservative
                                                                                                                                                                                                                            ; LOCATION: 1..717
US-08-465-485A-20
                                                                                                                                                                                                            NAME/KEY: CDS
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331 gicaacaaagaaaiggagcciiiggiggacaagiccaggaiiggaicgiggcciaccig 390
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APPLICANT: Tsujimoto, Yoshide;Croce, Carlo A.

TITLE OF INVENTION: DNA MOLECULES HAVING HUMAN BCL-2 GENE

;SEQUENCES
                                                                                                                                                                                                                                                                                                               3335-070-55 CONT
                                                                           APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION.
NAME: Fortney, Andrew D.
REGISTRATION NUBBER: 34,600
REFERENCE/DOCKET NUBBER: 3335-
TELECOMMUNICATION INFORMATION:
TELEFAX: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 717 base pairs
TYPE: nucleic acid
cTRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
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US-09-080-285-20
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5459251-1
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128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
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                                                                                             gggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtcc 367
                                                                                                                                                                                                                                                                        574 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG 633
                                                                                                                                                                                                                                                                                                                368 aggattggatcgtggcctacctggagacacgtctggctgactggatccacagcagtggcg 427
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                                                                                                                                                                                                                                                                                                                                                                                             getgggeggaetteacagetetatacggggaeggggeeetggaggaegeaeggegtetge 487
                                                                                                                                                                                                                                                                                                                                                                                                                              694 GCTGGGATACTÍTIGTGGAACTCTÁTGGGAÁCAATGCAGCAGCCGÁGAGCCGAAAGGGCC 753
                    188 gggaggcaactgggcatgagtgagcacagtggtgacgggggccg 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
STRET: P. O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARCD090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: CONCURRENTLY FILED
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/081.448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 22 JUNE 1993
ATTORNEY AGENT INFORMATION:
NAME: PARKER, David L.
REGISTRATION NUMBER: 32,165
REPREROKE/DOCKET NUMBER: ARCDC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
INFORMATION FOR SEC ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 926 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
135..836
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2IP: 77210
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LOCATION:
PCT-US94-07089-6
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                                                                                                                                                                                                                                                                                                              308 gggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtcc 367
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Length 926;
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ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
                                         Indels
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APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          488 gggagggcaactgggcatgagtgagcacagtggtgacgggggccg 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                754 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG 798
 Score 134.6; DB 6;
Pred. No. 4e-29;
0; Mismatches 169;
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APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/465,485A FILING DATE: 05-JUN-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20, Application US/08465485A Patent No. 5831066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Fortney, Andrew D. REGISTRATION NUMBER: 34,600
 23.2%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 22-DEC-1988 ATTORNEY/AGENT INFORMATION:
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                                         Matches 236; Conservative
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MEDIUM TYPE: Floppy
Ouery Match
Best Local Similarity
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CLASSIFICATION:
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Sequence 6, Application US/08470670A
Patent No. 5834309
Patent No. 5834309 5710045
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TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
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Best Local Similarity
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COCATION:
US-08-470-670A-6
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US-08-470-670A-6
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421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg
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Pred. No. 4e-29;
0; Mismatches 169; Indels 0
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STREET: 321 No. 5646008th Clark Street, Suite 800
CITY: Chicago
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,448
FILING DATE: 19930622
                                                                                                                                                   541 ggggccctggtaactgtaggggccttttttgctagcaag 579
                                                                                                                                                                                       541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
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APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
ATTORNEY/ABOTH INFORMATION:
NAME: NO. 5646008thrup, Thomas E.
REGISTRATION NUMBER: 33,268
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                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08081448 Patent No. 5646008
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Best Local Similarity 58.3%;
Matches 236; Conservative (
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TYPE: nucleic acid
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; LOCATION: 135..836
US-08-081-448-5
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368 aggattggatcgtggcctacctggagacacgtctggctgactggatccacagcagtggcg 427
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,670A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Thompson, Craig B. B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: ARCD:090--1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,448
FILING DATE: 22-JUN-1993
ATTORNEY AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642,000---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
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                ggggccctggtaactgtaggggccttttttgctagcaag 579
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IBM PC compatible
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91.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 85.6
Best Local Similarity 91.2
Matches 528; Conservative
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US-08-798-897-2
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US-08-978-523-2; Sequence 2, Application US/08978523; Patent No. 5883229

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                                                                                                      ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600 CITY: Washington
                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                             TITLE OF INVENTION: Genes Coding For Bcl-y, a TITLE OF INVENTION: Homologue
                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: ESEMOND, ROBERT W.
REGISTRATION UNDRER: 32,893
REFERENCE/DOCKET NUMBER: 1483
TELECOMMUNICATION INFORMATION:
TELEFAN: 202-371-2600
INFORMATION FOR SEQ ID NO: 2:
                  Guastella, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                     CORRESPONDENCE ADDRESS:
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EDNESS: both
                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: CDNA
US-08-978-523-2
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GENERAL INFORMATION
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                  APPLICANT:
                                                                                                                                                                            COUNTRY:
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ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
PTIENT NAME: PATENTINE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
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NAME: Esmond, Robert W.
REGISTRATION UNMER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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                                                                                                                     Length 579;
                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.
                                                                                                                  Score 540.6; DB 3;
Pred. No. 2.1e-143;
0; Mismatches 24;
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                      LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                  Query Match 93.0
Best Local Similarity 95.9
Matches 555; Conservative
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005
COMPUTER READABLE FORM:
                                                                        CDNA
                                                         ; TOPOLOGY: both
; MOLECULE TYPE: CD
US-08-978-523-1
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Sequence 16, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 22, Appl
Sequence 22, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
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Sequence 4, Appli
Sequence 2, Appli
Patent No. 5506344
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Patent No. 54
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Sequence 2
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-978-523-1
US-08-978-523-2
US-08-081-448-5
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PCT-US93-05551-4
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERRE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITT: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYZEH: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTONNEY/AGERT INFORMATION:
NAME: Essmond, Robert W.
REGISTRATION NUMBER: 32,893
REFRENCE/DOCKET NUMBER: 1483.0140001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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US-08-944-530-1
US-08-471-057-6
                    US-08-470-670A-8
PCT-US94-07089-8
US-08-471-058-20
US-08-112-208C-1
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US-08-37-646A-1
US-08-856-531-1
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US-08-866-034-1
US-08-871-058-8
US-08-471-058-8
US-08-471-057-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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APPLICANT: Guastella, John
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TYPE: nucleic acid
STRANDEDNESS: both
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336 AACTGAGGTACCGGAGGGCATTCAGTGACCTGACGTCCCAGCTCCACATCACCCCAGGGA 395

Page 10

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/db_xref="SPTREMBL:077737"
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AETPSAINGNPSWHLADSPAVNGATGHSSSLDAREVIPWAAVKQALREAGDEFELRYR
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VLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQERFNRWFLTGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="transmembrane domain: 680-736; Bcl-2 homolgy domains: BH4: 56-115, BH3: 298-343, BH1: 428-487, BH2: 581-628"
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                                   341 aaatggagcctttggtgggacaagtccaggattggatcgtggcctacctggagacacgtc 400
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                                                                        485 AGATGCAGGTATTGGTGAGTCGGATCGCAACTTGGATGGCCACTTACCTGAATGACCACC 544
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Artiodactyla; Suiformes; Suina; Suidae; Sus.
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/db_xref="G1:3288632"
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/db_xref="taxon:9823"
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Bartling, B.
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636 ATGCAGCAGCTGAGAGGCCGAGGACGCTTCAACCGATGGTTCCTGACGGCA 695
281 gccgtcttgtggcattctttgtctttggggctgcctgtgtgctgagagtgtcaacaaag 340
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/organism="Sus scrofa"
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2 (bases 1 to 926)
Boises, Gonzalez-Garcia, M., Postema, C.E., Ding, L., Lindsten, T.,
Turka, L.A., Mao, X., Nunez, G. and Thompson, C.B.
bcl-x, a bcl-2-related gene that functions as a dominant regulator
of apoptotic cell death
Cell 74 (4), 597-608 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /trānslation="MSQSNRELVVDFLSYKLSQKGYSWSQFSDVEBNRTEAPEGTESE
METSAINGNBSWHLADSPANGATHESSLDAREVIPMAANYGALREADBFEELRYR
METSBILTSCHITFGTAYQSFEQVVNELFRDGVNWGRIVAFFSFGALCVESVDKEMO
VLVSRIAAMMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQERFNRWFLTGM
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                                                                                                                                                                                                                                                                               Submitted (22-JUN-1993) Craig B Thompson, Howard Hughes Medical
Institute, University of Chicago, 5841 South Maryland, Chicago, IL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 AGCAAGCGTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGCATTCAGTG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 acctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccaggttt 247
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                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutherla;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 926)
Thompson, C. B.
                                                                                          26-JUL-1994
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Pred. No. 1.2e-21;
0; Mismatches 169; Indels
PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAA80661.1"
/db_xref="G1:510901"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="bcl-xL"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="brain"
135. .836
/gene="bcl-xL"
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/gene="bcl-xL"
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                                                                                        HSBCLXL 926 bp
H.sapiens bcl-xL mRNA.
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Z23115.1 GI:510900
bcl-xL gene.
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                                                                                                       DEFINITION
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TITLE
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ORIGIN
                                                             RESULT 13
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/translation="MSQSNRELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESE
AETPGAINDRSWHLADSPAVNGATHSSLDAREVIPMAANKQALREADBFELRYR
RAFSDLTSQLHITPGTASCEQVVNGHELFROGVNWGRIVAFFSFGALCVESYDKEM
VLVSRTATWMATYLNDHLEPPTQENGGWDTFVELYGNNAAESRKGQERFNRWFLTGM
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Submitted (13-DEC-1999) Biochemistry, SUNY at Buffalo, 3435 Main
Street, Buffalo, NY 14214-3000, USA
Location/Qualifiers
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                                                                             gctgggcggacttcacagctctatacggggacggggccctggaggacgcacggcgtctgc
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/protein_id="AAF33212.1"
/db_xref="G1:6959767"
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1 (bases 1 to 720)
Lee,T.L. and Canty,J.M.
PCR Cloning of a Porcine bcl-xL cDNA from Heart Unpublished
2 (bases 1 to 720)
                                                                                                                                                                                488 gggaggcaactgggcatgagtgagcacagtggtgacgggggccg 532
                                                                                                                                                                                                                             754 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG 798
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Pred. No. 1.6e-21;
0; Mismatches 188;
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RIVSNMTTYLTDHLDPWIQENGGWERFVDLYGNNAAAELRKGGETFNKWLLTGATVAG
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860. .1184
1161. .1166
324 c 374 g 237 t
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                                                                                                                                                                                                                                                                                                                               654 TTGTGTCTTGGATGACCAGGTACTTGACCAGACCATCTAGATCCCTGGATCCAGGAGAATG 713
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                                                                                                                                                                                                                                                                                                                                                                                                                                           714 GCGCTGGGAGCGCTTTGTGGATCTGTATGGGAACAACGCTGCTGCCGAGCTGAGGAAGG 773
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                                                                                                                                                                 125 tgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttct 184
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                                                                                                               Score 138.2; DB 4; Length 1184; Pred. No. 1.7e-22;
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                                                                                                                                        Indels
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                                                                                                                                       0; Mismatches 173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unclassified.

1 (bases 1 to 926)
Thompson,C.B., Boise,L.H. and Nunez,G.
Vertebrate apoptosis gene: compositions
Patent: US 5834309-A 6 10-NOV-1998;
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249 c 264 g
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                                                                                                               23.8%;
58.3%;
                                                                                                            Query Match
Best Local Similarity 58.3
Matches 242; Conservative
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454 ACCTGACATCCCAGGTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513
                                                     248 ccgacqaacttttccaaggggccctaactggggccgtcttgtggcattctttgtctttg 307
                                                                                                           514 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGCCCTTTTTCTCCTTCG 573
                                                                                                                                                                 gggctgcctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtcc 367
                                                                                                                                                                                                                          574 GCGGGGCCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG 633
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                                                                                                                                                                                                                                                                                                                                                                                                 428 gctgggcggacttcacagctctatacggggacgggccctggaggacgcacggggtctgc 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                          694 GCTGGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGAGCCGAGAGCCGAAAGGGCC 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 acctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccaggttt 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    368 aggattggatcgtggcctacctggagacacgtctggctgactggatccacagcagtggcg 427
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hompson, C.B., Boise, L.H. and Nunez, G.
Vertebrate apoptosis gene: compositions and methods
Patent: US 5646008-A 5 08-JUL-1997;
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Pred. No. 1.2e-21;
0; Mismatches 169; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    488 gggagggcaactgggcatgagtgagcacagtggtgacgggggccg 532
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152011
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249 c 264 q
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ral Similarity 58.3%;
236; Conservative (
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Best Local Similarity
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Direct Submission
Submitted (02-NOV-1994) J.A. Cruz-Reyes, National Institute of
Medical Research, NIMR/MRC Mill Hill, The Ridgeway Road, London NW7
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DLGSRALVEDLVRYKLCQRSLVPEPSGAASCALHSAMRAAGDEFEERFRQAFSEISTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Protein sequence is in conflict with the conceptual
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MVTYLETNLRDWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGAL
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                                                           caggittccgacgaactittccaaggggccctaactggggccgicttgtggcaitctit 300
                                                                                                                               gtctttggggctgcctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
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Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus
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/organism="xenopus laevis"
/db_xref="taxon:8355"
/dev_stage="28-30 (tailbud tadpole)"
/clone_lib="lambda ZapII:RI"
                                                                                                                                                                                                                                                                                                                                                                      VRT
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/db_xref="G1:1334682"
/db_xref="SWISS-PROT:091827"
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Cruz-Reyes,J. and Tata,J.R.
Cloning, characterization and
cell-survival genes
                                                                                                                                                                                                                                                                                                                                                                      mRNA
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3. .689
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3. 680
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African clawed frog.
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X82462
X82462.1 GI:575421
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Cruz-Reyes, J.A.
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AUTHORS
TITLE
                                                                241
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AUTHORS
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JOURNAL
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KEYWORDS
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Score 233.8; DB 4; Length 749; Pred. No. 1.2e-44;

40.2%; 68.1%;

Query Match Best Local Similarity

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/translation="MSSSNRELVIDFVSYKLSQRGHCWSELEEEDENRTDTAAEAEMD SVLNGSPSWHPPPAGHVVNGATVHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFS
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Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 1184)
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Direct Submission
Submitted (09-MAY-1995) Xavier Vilagrasa, Faculty of Medicine.
Submitted (09-MAY-1995) Xavier Vilagrasa, Faculty of Medicine.
University of Barcelona, Molecular Genetics Research Group,
Casanova 143, Barcelona 08036, Spain
On Sep 6, 1996 this sequence version replaced gi:1381039.
                                    aggeccagecgecgacecgetgeaceaagecatgegggetgetggagaegagtttgagae 164
                                                                                                               224
                                                                                                                            272 GCGATTCAGACAAGCATTCAGTGAGATCTCCACACAGTGATCATGTGACCCCCGGCACAGC 331
                                                                                                                                                                                     284
                                                                                                                                                                                                         285 tettgtggeattetttgtetttggggetgeeetgtgtgetgagagtgteaacaaagaaat 344
                                                                                                                                                                                                                                                                                               392 CATAGTTGCATTTTTGTTTTTGGTGCCGCGCTGTGTGCTGAGAGTGTCAACAAGGAGAT 451
                                                                                                                                                                                                                                                                                                                                   345 ggagcctttggtgggacaagtccaggattggatcgtggcctacctggagacacgtctggc 404
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0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              632 TGGAGCTGTGGCTCTGGGTGCTTTGATGACAGTAGGGGCCCTTGTTTGCCAGCAAGTG 688
                                                                                                               cogttccogccccttctctgacctggccgctcagctacacgtgaccccaggctcagc
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 Indels
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 Mismatches 152;
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/organism="Gallus gallus"
/strain="Hubbard White Mountain"
/db_xref="taxon:9031"
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/db_xref="GI:1522679"
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170. .859
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170. .859
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 Matches 325; Conservative
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VERSION
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43; Indels
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                                                                                                                                                 /standard_name="R94929"
                        /standard_name="H79035"
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161612. .161756
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al Similarity 90.1%;
390; Conservative (
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (26-021-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr cort 28, 1999 this sequence version replaced gi:4972127.

IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNS0000B 196287 bp DNA PRI 27-OCT-1999
Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-124D2 of
RPCI-11 library from chromosome 14 of Homo sapiens (Human),
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80431. .80564
                                                                                                                                                                                 agtggcggctgggcggacttcacagctctatacggggacggggcctggaggacgcacgg 480
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             300
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc
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78257. .78396
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Direct Submission
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/note="matching EMBL:AA167748; Identified using the software (G. Schuler)"
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Pred. No. 2.9e-75;
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107753. 107946
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| Oy 1 atgccgaccccagctccaaccccagacacacgcgctctagtggctgactttgtaggctat 60 | Oy 61 aggctgaggcagaaggttatgtctgtggagctggggcctggggaaggcccagccgccgac 120 | Oy 121 cogctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180  |  | 421 agtggcggctgggcgacttcacagctctatacggggacggggcctggaggacgcacgg 48   | 11 7 7 | RESULT 7   AR020780   579 bp   DNA   PAT   05-DEC-1998   | REFERENCE 1 (bases 1 to 579) AUTHORS Guastella, J. TITLE Genes coding for bcl-y a bcl-2 homologue JOURNAL Patent: US 5789201-A 2 04-AUG-1998; FEATURES Location/Qualifiers | Account 106 a 154 c 208 g 111 t c 208 g 111 | Qy   atgccgaccccagacacccagacacacgcgctctagtggctgactttgtaggctat 60   |
|--|--|--|--|---|--------|--|--|---|--|
| Oy 481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgaccgtgggcactg 540   | <pre>Qy 541 ggggccctggtaactgtaggggcctttttgctagcaagtg 581</pre>         | RESULT 6 D87461 3542 bp mRNA PRI 10-JUL-1997 DEFINITION Human mRNA for KIAA0271 gene, complete cds. ACCESSION D87461.1 GI:1944417 KEXWORDS KIAA0271. SOURCE Home sapiens male brain myloblast cell_line:KG-1 cDNA to mRNA, | Clone_lib:pSPORT 1 clone:HA6752.  ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.  Primates; Catarrhin1; Hominidae; Homo.  Primates; Catarrhin1; Hominidae; Homo.  AUTHORS Nomura, No.  JOURNAL Submitted (27-AUG-1996) to the DDBJ/EMBL/GenBank databases. Nobuo JOURNAL Submitted (27-AUG-1996) to the DDBJ/EMBL/GenBank databases. Nobuo JOURNAL Nomura, Kazusa DNA Research Institute, Gene Structure 1; 1532-3  Yana, Kisarazu, Chiba 292, Japan (E-mail:cdnainfo@kazusa.or.)  WRL.http://www.kazusa.or.in. Pdl:Ad38-52-3431, Pdl:Ad38-52-3431 | REFERENCE 2 (sites) AUTHORS Nagase, T., Seki, N., Ishikawa, R. and Nomura, N. TITLE Prediction of the coding sequences of unidentified human genes.VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of CDNA clones from human cell line KG-1 and brain Unpublished (1996) |        | MEDLINE 97191544  FEATURES  1. 3542  1. 3542  Ab_are="homo sapiens"  Ab_are="twon:9606"  Acell_ilne="kg-1"  Acell_type="myloblast"  Aclone="hA6752"  Asex="male" | /tissue_type="brain"  gene 177758 /gene="KIAA0271"  CDS 177758 /gene="KIAA0271" /note="similar to human transforming protein hol-2   | (A24428)" (A24428)" (Codon_start=1 /protein_id=BA19666.1" /db.xref="Gi:194418" /translation="MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGB AMRAAGDEFTRRRRFSDLAAGHTVPGSAGAGRFTQYSDELEGGGPNW GAALCAESVNKEMEPLVGQVGEWMVAYLETRLADWIHSSGGWAEFTALY RLREGNWASVRTVLTGAVALGALVTVGAFFASK"   | BASE COUNT       804 a       817 c       1030 g       891 t         ONEGIN       80 - 5%;       Score 502.6;       DB 9;       Length 3542;         Best Local Similarity       91.6%;       Pred. No. 3.6e-107;         Matches 532;       Conservative       0;       Mismatches 49;       Indels 0;       Gaps 0; |

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/note="promotes cell survival"
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/db_xref="taxon:9606"
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/map="14q11"
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Pred. No. 7e-116;
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Guastella, J.
Genes coding for bcl-y a bcl-2 homologue
Patent: US 5789201-A 1 04-AUG-1998;
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157 c 198 q
Sequence 1 from patent US
AR020779
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95.9%;
                     AR020779.1 GI:3975394
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RLREGNWASVRTVLTGAVALGALYTVGAFFASK"
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Gibson, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 582)
Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G., Denkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S. bcl-w, a novel member of the bcl-2 family, promotes cell survival Oncogene 13 (4), 665-675 (1996)
                                                                                                                                                                                                                                             Cory,S.
Direct Submission
Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia
Location/Qualifiers
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Hammer.S. Skoglosa,Y. and Lindholm,D.
Direct Submission
Submitted (01-0CT-1998) Developmental Neuroscience, Uppsala
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 582)
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Differential expression of Bcl-w and Bcl-x mRNA in and adult nervous system
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Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds.
AF096291
                                                                                      Indels
       /note="mRNA destabilization element" 3428. :3441 / gene="BG1-w" 814 c 991 g 875 t
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                                                               96.4%; Suc. 97.8%; Pred. No. ... 97.8%; O; Mismatches
/gene="Bcl-w"
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                                                                   Query Match
Best Local Similarity 97.8
Matches 568; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Norway rat.
Rattus norvegicus
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gaalcaesvnkemeplvgqvqdmwytyletrladwihssggwaeftalygdgaleear
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                                                      /organism="Rattus norvegicus"
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                                                                                                                                                                                                 /gene="bcl-w"
/note="Bcl-2 family member"
                                                                   /strain="Sprague_Dawley"
/db_xref="taxon:10116"
/tissue_type="brain"
/dev_stage="postnatal"
1..582
                                                                                                                                                                                                                                                                          /protein_id="AAC64200.1"
/db_xref="GI:3747130"
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/product="BC1:1572495"
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AMRAGDEFETREFREMEDLYGOVQDMWTAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
GAALCAESWNREMEDLYGOVQDMWTAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
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Gibson, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and
                                                                                                                                                            1 (bases 1 to 52), December 1 to 52), Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S. Obcl-w, a novel member of the bcl-2 family, promotes cell survival 0ncogene 13 (4), 665-675 (1996)
                                                                                                                                                                                                                                                                                                                                     Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia Location/Qualifiers
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="bcl-w"
/note="promotes cell survival; Bcl-2 homolog"
                                   Mus musculus Bcl-w (bcl-w) mRNA, complete cds. U59746
                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_line="BaF3"
1. .582
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/translation="MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
AARAAGDEFETRRRRFSDLAAQLHYPGSAQQRFTQYSDELPQGGPWGRLVAFFVF
GAARAAGDEFETRRRRFSDLAAQLHYPGSAQQRFTQYSDELPGGGPWGRLVAFFVF
FLREGNWASVRFVLTGAVALGALVTVGAFFASK"
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MacGregor, G.R.
aging agradic and a control of the c
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3476)
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Submitted (21-OCT-1997) Center for Molecular Medicine, Emory
University, 1462 Clifton Road, Atlanta, GA 30322, USA
Location/Qualifiers
                                                                                                                                                   caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc
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Mus musculus BCL-W (Bcl-W) mRNA, complete cds.
AF030769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bcl-w is required for testis homeostasis
Unpublished
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/db_xref="GI:2623250"
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/chromosome="14"
/map="19.5 cM"
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Ross, A.J. and MacGregor, G.R.
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/gene="Bcl-w"
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/gene="Bcl-w"
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

July 4, 2000, 01:21:54; Search time 888.39 Seconds (without alignments)
-636.198 Million cell updates/sec

Run on:

1 atgoogaccccagcctcaac.....gccttttttgctagcaagtg 581 US-09-155-327B-8 581 Title: Perfect score: Sequence:

Scoring table:

882769 seqs, -486395729 residues IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Searched: 1765538

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Databas

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|           | Description    |          | _              | Mus mus | rarras<br>Common | ARUZU//9 Sequence |            | 1200010 Human mknA | v    | 829 Human |     | allus g  | $^{\circ}$ | Š      | Ξ       | AF216205 Sus scrof | AJ001203 Sus scrof | U10579 Rattus norv | U72350 Rattus norv | X82537 R.norvegicu |     |     | S76513 bcl-x=apopt | U72398 Human Bc1-x | 18 Homo  | <br>Z  | U92434 Bos taurus | M.mu | Mus   | Mus muscul | ns muscul | 26 Eukary | 72 Sequenc | υ    | sedneuc  | og sednenc | Human B-C | Sequence 1 | M14745 Human bcl-2 | ~        | AR021160 Sequence | 60       | X06487 H.sapiens m | G      | R054019 Sequenc | 0      | U72349 Rattus norv |
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| SUMMARIES | ID             | 1.000000 | ACOMM<br>10001 | AF03076 | AF09029          | -                 | #15000H    | D8/461             | ₫,   |           |     | GGU26645 | 7          | 152011 | HSBCLXL | AF216205           | SSJ001203          |                    |                    |                    |     |     |                    |                    | AC016218 |        | ш                 |      |       | MUSBCLX    | MMU5127   | AF060226  | ARU52622   |      | ARU52621 | AK054008   | HUMBCL2A  | I08038     | HUMBCL2C           | RATBCL2A | AR021160          | AR054009 | HSBCL21G           | GGBCLX | AR054019        | 152010 | RNU72349           |
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|           | Query<br>Match |          | 4.             | 4.6     | 2                | 7 0               | ٠,         | . ה                | n i  | 2.7       | 0.5 |          |            |        | 3.2     |                    |                    |                    |                    | •                  | •   |     | •                  |                    |          | ٠      |                   |      | 1.8   | ٠          |           | œ :       | ٠          | •    |          |            |           |            |                    |          |                   |          |                    | 7.0    |                 | 0.7    | •                  |
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND (POTENTIAL).
-!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH
HIGHEST LEVELS IN THE HEART AND SKELETAL WUSCLE.
-!- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIR, BID, BAK AND BAX FOR
THEIR KILLING ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-
--- APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-!- SIMILARITY: CONTAINS B BCL-2 HOMOLOGY DOMAIN 3 (BH3).
                                                                                                                                                                                                                                                                                                                                                                               Chittenden T., Harrington E.A., O'Connor R., Flemington C., Lutz R.J., Evan G.I., Guild B.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG EIB 19K PROTEIN.
-1- SUBUNIT: FORMS HETERODIMERS WITH BCL-2, EIB 19K PROTEIN, AND BCL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 96091131.
Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J., Elamingvan B., Chinnadurai G., Lutz R.J.;
A conserved domain in Bak, distinct from BH1 and BH2, mediates cell death and protein binding functions.";
EMBO J. 14:5589-5596(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Modulation of apoptosis by the widely distributed Bcl-2 homologue
                                                                                                                                                                                                                                  Grinham C.J., Martinou J.C., Brown R.;
"Cloning of a bcl-2 homologue by interaction with adenovirus E1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 97172562.
Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J.E., Sattler M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J., Thompson C.B., Fesik S.W.;
"Structure of Bcl-xL-Bak peptide complex: recognition between
                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 95231654.
Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R.,
Tomei L.D., Barr P.J.;
01-NOV-1997 (Rel. 35, Last annotation update)
BCL-2 HOMOLOGOUS ANTAGONIST/KILLER (APOPTOSIS REGULATOR BAK).
                                                                                                                                                                                                               Farrow S.N., White J.H.M., Martinou I., Raven T., Pun K.-T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eguch1 H., Hayash1 S.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                   "Induction of apoptosis by the Bcl-2 homologue Bak."; Nature 374:733-736(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND FUNCTION OF BH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 96-206 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 374:736-739(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulators of apoptosis."
Science 275:983-986(1997)
                                                                                                                                                                                                                                                                                               Nature 374:731-733(1995)
                                                              Homo sapiens (Human)
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                             BAK1 OR BAK.
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-i-DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK AND BAX FOR THEIR KILLING ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
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-i-SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-i-SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 GDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIATSLFESGINWGRVVALLGFGYRLALH 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN.
-1- SUBUNIT: FORMS HETERODIMES WITH BCL-2, E1B 19K PROTEIN, AND BCL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 GDEFETRFRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Modulation of apoptosis by the widely distributed Bcl-2 homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
BCL-2 HOMOLOGOUS ANTAGONIST/KILLER 2 (APOPTOSIS REGULATOR BAK-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin1; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 SVNKEMEPLVGQVQDWIVAY-LETRLADWIHSSGGWADFTALYGDGAL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 VYQHGLTGFLGQVTRFVVDFMLHHCIARWIAQRGGWVAALNL-GNGPI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 235; DB 1; Length 211
Pred. No. 1.42e-26;
26; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - SUBCELLULAR LOCATION; MEMBRANE-ASSOCIATED (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23409 MW; A2200FE72A46D04E CRC64;
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apoptosis; Transmembrane; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                   PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS0062; BH3; 1.
PROSITE; PS50062; BC12_FAMILY; 1.
PFAM; PF00452; BC1-2; 1.
                                                                                            EMBL, U23765, AAA93066.1; --
RMBL, UB811, AAA74466.1; --
EMBL, D88397, BAA13606.1; --
EMBL, D88396; BAA13606.1; JOINED.
                                                               EMBL; X84213; CAA58997.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 32.4%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 374:736-739(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                      PDB; 1BXL; 29-OCT-97.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95231654
                                                                                                                                                                                                                                                                          600516; -
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Q13014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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STIFFF SON REPRESENTATION OF THE PROPERTY OF T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLGAYL
                                                                                                                                        -1- FUNCTION: PROLONGS THE SURVINGL OF HEMATOPOIETIC CELLS IN THE ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULARN BEATH. BCL2 BLOCKS APOPTOSIS BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY PREVENTING THE RELEASE OF CYTOCHROME C. MIGHT FUNCTION IN AN ANTIOXIDARY PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 VATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 RDCVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 QGGPNWGRLVAFFYFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADF 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GHK -> VGACLVE (IN ISOFORM BCL-2-BETA)
AA85EF6B0766BE0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01260; BH4_1; 1.
PROSITE; PS50063; BH4_2; 1.
PRAM, PF00452; Bc1-2; 1.
Apoptosis; Alternative splicing; Transmembrane; Mitochondrion. DOMAIN 10 30 BH4.
                                                                                                                                                                                                                                                                                                                             -i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 VELYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
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Pred. No. 3.72e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
Nucleic Acids Res. 20:4187-4192(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, L31532, AAA37282.1; -.
EMBL, M16506; AAA37282.1; JOINED.
EMBL, M16506; AAA37281.1; -.
PIR, A25960; TYMSA1.
PIR, B25960; TYMSB1.
PIR, B37332, E37332.
HSSP, Q07817; IMAZ.
MGD, MGI:88138; BCL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50062; BCL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01259; BH2; 1.
PROSITE; PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 AA; 26425 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 40.0%;
Best Local Similarity 43.4%;
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                    FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 GEGATQGIVEEEVLQALLEATEEFELRYQRAFSDLTSQLHITQDTAQQSFQQVMGELFRD 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 GINWGRIVAFFSFGRALCVESANKEMTDLLPRIVQWMVNYLEHTLQPWMQENGGWEAFVG 165
                                                                                                                                                                                                                                                                          2; Gaps
                                                                                                                                                                                                                                                 Cruz-Reyes J., Tata J.R.; "Cloning, characterization and expression of two Xenopus bcl-2-like
                                                                                                                             APOPTOSIS KEGULATOR KII (XKII).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31; Mismatches 48; Indels
148 TALYGDGALEDARRLREGNW-AVSTVVTGAVALGALVTVGAFFASK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 AA; 23379 MW; 3BFC6BE6DDA4CA03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 546; DB 1;
Pred. No. 2.78e-96;
                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAK_HUMAN
(1661): (092533;
01-N0V-1997 (Rel. 35, Created)
01-N0V-1997 (Rel. 35, Last sequence update)
                                                     204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 LYGDGALEDARRIREG-NWAVSTVV-TGAVAL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 LYGKNAAAQSRESQERFGRLLTIVMLTGVFAL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
PFAM; PF00452; BCl-2; 1.
Apoptosis; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BH1.
                                                                                                                        APOPTOSIS REGULATOR R11 (XR11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X82461; CAA57844.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 39.4%;
Local Similarity 46.7%;
Les 71; Conservative
                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167
                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                    MEDLINE; 95331613.
                                                                                                                                                                                                                        TISSUE=HEAD
                                       T 13
AR11_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                               Xenopus.
                                                                    091828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                          RESULT
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                                                                                                                                                                                                                                                                                                                                                                             -1- FUNCTION: PROLÒNGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLCCKS APOPTOSIS BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY PREVENTING THE RELEASE OF CYTOCHROME C. MIGHT FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.
                                                                                                                                                          Hockenbery D., Nunez G., Milliman C., Schreiber R.D., Korsmeyer S.J.; "BG1-2 is an inner mitochondrial membrane protein that blocks programmed cell death."; Nature 348:334-336(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ALSO KNOWN AS TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: MITOCHONDRIAL INNER AND OUTER MEMBRANES, AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND BAK PROFEINS, AND WITH BCL-X(S). HETERODIMERIZATION WITH BAX REQUIRES INTACT BH1 AND BH2 DOMAINS, AND IS NECESSARY FOR ANTI-APOPTOTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WELL AS NUCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM.

-!- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TERMINAL ENDS.

-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.

-!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               II CHRONIC LYMPHATIC LEUKEMIA) BY A CHROMOSOMAL TRANSLOCATION T(14;18)(Q32;Q21) WHICH INVOLVES BCLZ AND IMMUNOGLOBULIN GENE
                ranaka S., Louie D.C., Kant J.A., Reed J.C.;
"frequent incidence of somatic mutations in translocated BCL2
oncogenes of non-Hodgkin's lymphomas.";
Blood 79:229-237(1992).
                                                                                                                                                                                                                                                                          MEDILNE; 94239528.
Yin X.-M., Oltvai 2.N., Korsmeyer J.;
"BH1 and BH2 domains of Bcl-2 are required for inhibition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISEASE: INVOLVED IN FOLLICULAR LYMPHOMA (FL)
                                                                                                                                                                                                                                                                                                                                          apoptosis and heterodimerization with Bax."; Nature 369:321-323(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M13994; AAA51813.1; ALT_SEQ.
EMBL; M13995; AAA51814.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD14111.1; ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X06487; CAA29778.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M14745; AAA35591.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR, A29409; TVHUA1.
PIR, B29409; TVHUB1.
PIR, A24428; TVHUBC.
PIR, C37332; C37332.
PIR, D37332; D37332.
HSSP, P53563; IAF3.
MIM, 151430;
                                                                                                                     SUBCELLULAR LOCATION.
MEDLINE; 92096610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS50062;
                                                                                                                                      MEDLINE; 91066924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S72602;
                                                                                                                                                                                                                                                           MUTAGENESIS
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LOSS OF ANTI-APOPTOTIC ACTIVITY.
W->A: NO HETERODIMERIZATION WITH BAX, AND
LOSS OF ANTI-APOPTOTIC ACTIVITY.
                                                                                                                                                                                                                                              /FTIG-VAR_000828.
V -> I (IN NON-HODGKINS-LYMPHOMA; SOMATIC
MUTATION).
                                                                                                                 POTENTIAL.
DAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLGAYL
                                                                                                                                         GHK -> VGASGDVS (IN ISOFORM BCL-2-BETA).
G->A: NO HETERODIMERIZATION WITH BAX, AND
                                                                                                                                                                                                                    /FTId-VAR_000827.
P -> S (IN NON-HODGKINS-LYMPHOMA; SOMATIC
                                                                                                                                                                                                                                                                                                                                                                                                                                            81 AAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELFRD 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 92375724.

Eguchi Y., Ewert D.L., Tsujimoto Y.;

Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 GVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAFVE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Negrini M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.; "Molecular analysis of mbcl-2: structure and expression of the murine gene homologous to the human gene involved in follicular lymphoma.";
          PFAM; PF00452; Bcl-2; 1.
Proto-oncogene; Apoptosis; Alternative splicing; Transmembrane; Mitochondrion; Chromosomal translocation; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                          , marcn 40.1%; Score 556; DB 1; Length 239;
Local Similarity 43.3%; Pred. No. 1.27e-98;
les 71; Conservative
                                                                                                                                                                                                                                                                                                            I -> F (IN REF. 4).
P -> T (IN REF. 3).
S -> R (IN REF. 3).
R -> C (IN REF. 4).
W; 3C49F2B714DC9CCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 LYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 239
                                                                                                                                                                                                                                                                                          MUTATION).
/FTId=VAR_000829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCL2_MOUSE STANDARD; PRT; 236 AA. P10417; P10418; 01-MAR-1989 (Rel. 10, Created) 01-APR-1993 (Rel. 25, Last sequence update) 15-UL-1998 (Rel. 36, Last annotation update) APOPTOSIS REGULATOR BCL-2.
                                                                                                                                                                                                                                                                                                             48 I
59 P
117 S
129 R
26266 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BALB/C; TISSUE-LIVER; MEDLINE; 87187643.
PROSITE; PS50063; BH4_2; 1.
                                                             30
107
155
202
233
233
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                                                                                                                                                                                                                                                                                                             48
59
117
129
139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                   Disease mutation
                                                                                                                                                     145
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                                                                                                                                                                                                                                                                         93
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                                                                                                     DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                             CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                              VARSPLIC
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                                                                                                                                                      MUTAGEN
                                                                           DOMAIN
                                                                                                                                                                                MUTAGEN
                                                                                                                                                                                                        VARIANT
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                                                                DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERATION SUCH AS MITOCHONDRIA.

SUBUNTI: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND BAR PROTEINS, AND WITH BALLA (S.). HETERODIMERIZATION WITH BAX REQUIRES INFACT BH1 AND BH2 DOMAINS, AND IS NECESSARY FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY).

SUBCELLULAR LOCATION: MITOCHONDRIAL INNER AND OUTER MEMBRANES, AS WELL AS NUCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM.

ALTERNATIVE PRODUCTS: TWO FORMS OF BGL. 2: ALDHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
                                                                                                                                               STRAIN-SPRAGUE-DWALEY, TISSUE-OVARY,
MEDLINE; 95120487.
Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
FEXPRESSION of members of the bcl-2 gene family in the immature rat
ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
cell apoptosis is associated with decreased bax and constitutive
bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
Endocrinology 136:232-241(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY PREVENTING THE RELEASE OF CYTOCHROME C. MIGHT FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRANULE AND PYRAMIDAL NEURONS OF HIPPOCAMPUS, PONTINE NUCLEI, CEREBELLAR GRANULE NEURONS, AND IN EPENDYMAL CELLS. IN PRENATAL BRAIN. EXPRESSION IS HIGHER AND LOCALIZED IN THE NEUROEPITHELIUM AND IN THE CORTICAL PLATE.

DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
                                Sato T., Irie S., Krajewski S., Reed J.C.; "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein."; Gene 140:291-292(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOLETIC CELLS IN THE ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULAR DEATH, BCL2 BLOCKS APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                            'bcl-2 messenger RNA is localized in neurons of the developing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIFFER AT THEIR C-TERMINAL ENDS.
TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES, WITH
HIGHEST LEVELS IN REPRODUCTIVE TISSUES. IN THE ADULT BRAIN,
EXPRESSION IS LOCALIZED IN MITRAL CELLS OF THE OLFACTORY BULB,
                                                                                                                                                                                                                                                                                                                                                                                            Castren E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOWAIN 1 (BH1).
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOWAIN 3 (BH3).
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOWAIN 4 (BH4).
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50062; BCL2_FAMILY; 1. PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1. PROSITE; PS01259; BH3; 1. PROSITE; PS01260; BH4_1; 1. PROSITE; PS50063; BH4_2; 1. PROM; PF00452; BCl-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuroscience 61:165-177(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L14680; AAA53662.1; -.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 19-172 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; S74122; CAB33200.1; -. HSSP; P53563; 1AF3.
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                       MEDLINE; 94193015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adult rat brain.";
                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                              95059917
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LISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                          Lindholm D.;
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE;
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Eguchi Y., Ewert D.L., Tsujimoto Y.; "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 VANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE; 87002488.
Cleary M.L., Smith S.D., Sklar J.;
"Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin transcript resulting from the t(14;18) translocation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87
                                                                                                                                                                                                                                                                                                                                                                                                               6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2-Ig fusion gene in lymphoma.";
EMBO J. 7:123-131(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tsujimoto Y., Croce C.M.; "Analysis of the structure, transcripts, and protein products of bol-2, the gene involved in human follicular lymphoma."; Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
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splicing; Transmembrane; Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                    556; DB 1; Length 236; No. 1.27e-98;
                                                                                                                                                                                                                                                                                                                                                                                                            45; Mismatches 43; Indels
                                                                                                                                                                    A -> R (IN REF. 2).
E -> G (IN REF. 1).
S -> Y (IN REF. 2).
L -> O (IN REF. 2).
W, E7688CB9071A872A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 VELYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P10415; P10416; Q16197; Q13842;
01-MAR-1989 (Rel. 10, Created)
101-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 AA
                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                    Score 556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 20:4187-4192(1992)
                                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                212 L
26622 MW;
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                                                                                                                                                                                                                                                                                                                                                    40.18;
                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 43.4%;
nes 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APOPTOSIS REGULATOR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
   Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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BCL2_HUMAN
   Apoptosis;
                                                                                                                                                                       CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                              TRANSMEM
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                        DOMAIN
DOMAIN
DOMAIN
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SEQUENCE FROM N.A.
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TRANSMEM
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Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eguchi Y., Ewert D.L., Tsujimoto Y.;
"Isolation and characterization of the chicken bol-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.";
                                                                                                                                                                                                                                                                                                            145 SFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
                                                                                                                                                                                                                                                                                                                                                                               SIMILARLIY).
SUBCELLULAR LOCATION: MITOCHONDRIAL INNER AND OUTER MEMBRANES, AS
WELL AS NUCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM (BY
                                                                                                                                                                                                                                                                                      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVLNELFRDGVNWGRIVAFF 144
                                                                                                                                                                                                                                                     3; Gaps
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                                                                                                                                                                                                              Score 613; DB 1; Length 233;
Pred. No. 4.92e-112;
35; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
                                                                                                                                                                               18BF6FA0441912B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
APPPPOSIS REGULATOR BCL'-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 AA.
                  PROSITE; PS01260; BH4_1; 1.
PROSITE; PS5003; BH4_2; 1.
PROSITE; PS500452; BC1-2; 1.
Apoptosis; Mitochondrion; Transmembrane.
                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 20:4187-4192(1992).
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                                                                                                     86 100 BH3
129 148 BH1
180 195 216
210 226 POT
233 AA; 26061 MW; 1
BH3; 1.
BH4_1; 1.
BH4_2; 1.
                                                                                                                                                                                                                / Match
Local Similarity 51.7%;
hes 75; Conservative
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Gallus gallus (Chicken).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92379084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
 PS01259;
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Q00709;
                                                                                                                                                              TRANSMEM
SEQUENCE
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                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 ORDFAOMSGOLHLTPFTAHGRFVAVVEELFRDGVNWGRIVAFFFFGGVMCVESVNREMSP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 LVDNIATWMTEYLNRHLHNWIQDNGGWDAFVELYGN-SM---RPLFDFSWISLKTILSLV 218
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 561; DB 1; Length 233; Pred. No. 8.52e-100;
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5252555ACB6E4C3D CRC64;
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GSAAASEVPPAEGLRP ->
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H -> T (IN REF. 2).
G -> V (IN REF. 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apoptosis; Transmembrane; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D11382; BAA01978.1; -.
EMBL; D11381; BAA01978.1; JOINED.
EMBL; Z11961; CAA78018.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВНЗ.
ВН1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4_1; 1.
PROSITE; PS50063; BH4_2; 1.
PFAM; PF00452; BC1-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APOPTOSIS REGULATOR BCL-2.
BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 LVGACITLGAYLGHK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|| :|:||::|
178 ALGALVTVGAFFASK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30
101
149
228
64
64
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PIR; S24390; S24390.
HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 1
233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
101 VFGAALCAESVNKEMEPLVGQVQDMIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T., Turka L.A., Mao X., Nunez G., Thompson C.B.;
"bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic cell death.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOI. REPLOG. DEV. 47:26-29(1997).

-1- FUNCTION: DOMINNAT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG FORM DISPLASS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE (BY SIMILARITY).

-1- ALTERNATIVE PRODUCTS: A LONG ISOFORM (SHOWN HERE) AND A SHORT ISOFORM ARE PRODUCTS: A LONG ISOFORM (SHOWN HERE) AND A SHORT ISOFORM AND PRODUCTS: A LONG ISOFORM (SHOWN HERE) AND A SHORT ISOFORM AND PRODUCTS: A LONG ISOFORM (SHOWN HERE) AND A SHORT ISOFORM AND PRODUCTS: A LONG ISOFORM SHORT ISOFORM SHORT ISOFORM AND PRODUCTS: A LONG ISOFORM SHORT ISOFORM AND PRODUCTS: A LONG ISOFORM SHORT SHOR
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-I- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY).

-I- SIMILARITY: CONTAINS A BCL-2 HOWOLOGY DOMAIN 1 (BH1).

-I- SIMILARITY: CONTAINS A BCL-2 HOWOLOGY DOMAIN 2 (BH2).

-I- SIMILARITY: CONTAINS A BCL-2 HOWOLOGY DOMAIN 3 (BH3).

-I- SIMILARITY: CONTAINS A BCL-2 HOWOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vilagrasa X., Mezquita C., Mezquita J.;
"Differential expression of bcl-2 and bcl-x during chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apoptosis; Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                  BCLX_CHICK STANDARD; PRT; 229 AA. 007815; 098908; 01-FFB-1995 (Rel. 31, Created) 11-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-HUBBARD WHITE MOUNTAIN; TISSUE-TESTIS; MEDLINE; 97264485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50062; BCL2 FAMILY; 1. PROSITE; PS01080; BH1; 1. PROSITE; PS01289; BH2; 1. PROSITE; PS01259; BH3; 1. PROSITE; PS01260; BH4_1; 1. PROSITE; PS50063; BH4_2; 1.
                                                                                                                                     205 KGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                         ::| | | ::: | | |::| | ||:| | ||:| | ||:| | ||:| | ||:| | ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE FROM N.A. (LONG FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z23110; CAA80657.1; -. EMBL; U26645; AAB07677.1; -.
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BCL2L1 OR BCLX OR BCL-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell 74:597-608(1993).
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Mol. Reprod. Dev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
ERFYDLYGNNAAAELRKGQETFNKWLLTGATVAGVLLLGSL
                                                                                                                                                                                                                                                                  79 ASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFHDGVNWGRIVA 138
                                                                                                                                                                                                                                                   139 FFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDPWIQENGGWERFVDLYGNNAAAE 198
                                                                                                                                                                                                        3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.; "Expression of apoptosis-associated genes in hibernating and stunned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE (BY SIMILARITY).
-i- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC FUNCTION. INTACT AND BH2 DOMAINS ARE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                     LSRK -> VRTALP (IN SHORT ISOFORM)
A97D3A4D04C0E9DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Sulna; Suidae; Sus.
                                                                                                                                                             36; Indels
                                                                                                                              Length 229;
                                                                                                                                 Score 620; DB 1; Le Pred. No. 1.09e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                              33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    233 AA
                                                                                                                                                                                                                                                                                                                             199 LRKGQETFNKWLLTGATVAGVLLLGSLLS 227
                             BH1.
BH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ001203; CAA04597.1; -. PROSITE; PS50062; BCL2_FAMILY; 1. PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999 (Rel. 38, Created)
                                                                                                   229 AA; 25733 MW;
                                                                                                                                Match 44.7%;
Local Similarity 51.7%;
es 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APOPTOSIS REGULATOR BCL-X.
                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BCL2L1 OR BLC2L OR BCLX.
24
96
144
191
223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                   LT 8
BCLX_PIG
077737;
                           DOMAIN
DOMAIN
TRANSMEM
                                                                                                   SEQUENCE
                                                                                                                                 Query Match
                                                                         VARSPLIC
                DOMAIN
                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                    :: ||:| |||||| |:||:|||::|||::|||:||| | | ||:|||:||| | ||||:|||| 41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVIPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100
                                                                                                                                                                                                                                                                                                                                                                                               Grillot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N., Ohta S., Seldin M.F., Nunez G.;
"Genomic organization, promoter region analysis, and chromosome localization of the mouse bcl-x gene.";
"Immunol. 158:4750-4757(1997).
-I- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG FORM AND THE DELTA-TM FORM DISPLAY CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT ISOFOWN PROMOTES APOPTOSIS (BY SIMILARITY).
-I- SUBBUIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS BCL-X(S) FORMS HETERODIMERS WITH BAZ AND BAK, WHEREAS
                                                                                                                                                                                                                85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
                                                                                                                                                                                                                                                                                                                                                       145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
                                                                                                                                              3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fang W., Rivard J.J., Mueller D.L., Behrens T.W.; "Cloning and molecular characterization of mouse bcl-x in B and T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang X.-F., Weber G.F., Cantor H.; A novel Bol.x isoform connected to the T cell receptor regulates apoptosis in T cells." Immunity 7:629-639(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thompson C.B., Nunez G.; "Double The major Dolor," The major Dolor, making murine development and its product localizes to mitochondria."; Development 120:3033-3042(1994).
                                                                     44.9%; Score 623; DB 1; Length 233;
                                                                                                                                       34; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (X(L); X(S) AND X(DELTA-TM) ISOFORMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=2A4B;
Kamesaki H., Michaud G.Y., Takatsu K., Okuma M.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
233 AA; 26049 MW; E09D3CDD851AE9BE CRC64;
                                                                                                  Pred. No. 2.13e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCLX_MOUSE STANDARD; PRT; 233 AA. 064373, 266657, 2666581, 2661338; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) BCL2L1 OR BCL2L OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (X(L) AND BETA ISOFORMS).
STRAIN-C57BL/6; TISSUE-BRAIN;
MEDLINE; 95331139.
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STRAIN-C57BL/6 X CBA; TISSUE-THYMUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 KGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::| | | ::: | | | ::
161 RLREG-N-WAVSTV-VTGAVALGAL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lymphocytes.";
J. Immunol. 153:4388-4398(1994).
                                                                                                      Best Local Similarity 52.4%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-PRE-B CELL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 98051053.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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   SEQUENCE
                                                                         Ouery Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ñ
                                                                                                                                                                 MISSING (IN ISOFORM BCL-X(S)).
DIFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSRK -> VRTTPLVCPPLACVSLLCEHP (IN ISOFORM BCL-X-BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSLFSRK
-> GHDCGWCGSAGLTLQSEVTRH (IN ISOFORM BCL-
                                                                                                      TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN THE BRAIN, THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) AND BCL-X(DELTA-TM) EXPRESSION IS ENHANCED IN B AND I LYMPHOCYTES THAT HAVE BEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 204
                                            ENVELOPE FOR BCL-X(L), CYTOPLASMIC FOR BCL-X(DELTA-TM).
ALTERNATIVE PRODUCTS: FOUR ISOFORMS, BCX-X(L) (SHOWN HERE), BCL-X(S), BCL-X-BETA AND BCL-X(DELTA-TM), ARE DERIVED BY ALTERNATIVE
BAX DOES NOT SEEM TO BE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Gaps
                                 SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apoptosis; Mitochondrion; Alternative splicing; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.9%; Score 623; DB 1; Length 233; 52.4%; Pred. No. 2.13e-114;
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EMBL; L35049; AAA51039.1; -.
EMBL; L35048; AAA51040.1; -.
EMBL; U10102; AAA82174.1; -.
EMBL; U10101; AAA82173.1; -.
EMBL; U10100; AAA82172.1; -.
EMBL; U78031; AAC53460.1; -.
EMBL; U78031; AAB96881.1; -.
EMBL; U78031; AAB96881.1; -.
EMBL; U78031; AAB96881.1; JOINED.
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PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
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Matches 76; Conservative
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                    101 VFGAALCAESVNKEMEPLVGQVQDMIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160
                                                                                                                                                                                                                                                                                                                              85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
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                                                                                                                                                                                                                                                  Gaps
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BEDLINE; 9336497.

Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,

Turka L.A., Mao X., Nunez G., Thompson C.B.;

Turka L.A., Mao X., Nunez G., Thompson C.B.;

The Dept. Second Seco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 97172562.
Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J.E.,
Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
Thompson C.B., Fesik S.W.;
"Structure of BCL-xL-Bak peptide complex: recognition between
regulators of apoptosis.";
Science 275:983-986(1997).
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                                                                                                                                                                                          Score 623; DB 1; Length 233;
                                                                                                                                                                                                                                            34; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inohara N., Ohta S.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                 2B62B6C63864BC8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Bax-independent inhibition of apoptosis by Bcl-XL.";
I -> L (IN REF. 4).
A -> V (IN REF. 4).
FF -> SS (IN REF. 4).
A -> T (IN REF. 4).
A -> P (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995)
                                                                                                                                                                                                                Pred. No. 2.13e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    007817; 092976;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOP-1997 (Rel. 32, Last annotation update)
BCL2L1 OR BLC2L OR BCL.X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 KGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUTAGENESIS OF BH1 AND BH2 DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (BETA ISOFORM).
                                                                                                                                 26158 MW;
                                                                                                                                                                                       Similarity 52.4%; 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE BY NMR OF 1-209.
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81
119
143
199
201
233 AA;
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                                                                                                                                                                                                                      Best Local Similarity
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                         CONFLICT
CONFLICT
CONFLICT
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 MISSING (IN ISOFORM BCL-X(S)).
DTFVELYGNNAAAESRKGQERENRWFLTGGWYAGVYLLGSL
FSRK -> VRTKPLVCPFSLASGGRSFTALLLYLFLLCWYI
FYGUUS (IN ISOFORM BCL-X(BETA)).
FRD->VRA: NO HEFERODIMERIZATION WITH BAX.
VNW->AIL: LOSS OF ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G->A: NO HETERODIMERIZATION WITH BAX.
G->E: NO HETERODIMERIZATION WITH BAX.
WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY
BY ABOUT HALF.
                                                                                                                                                                                                                                                                                                                                                                                 ATA, 20037, PROSTIE; PS50062; BCL2_FAMILY; 1.
PROSTIE; PS01080; BH1; 1.
PROSTIE; PS01258; BH2; 1.
PROSTIE; PS01259; BH3; 1.
PROSTIE; PS01260; BH4 1; 1.
PROSTIE; PS00663; BH4 2; 1.
ADPOPTOSIS; Mitochondrion; Alternative splicing; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRI->ELN: LOSS OF ANTI-APOPTOTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTIVITY.
                                                                                                                                                                                                                                                                                                                         EMBL, 223116; CAA80662.1; --
EMBL, 223115; CAA80661.1; --
EMBL, U72398; AB1754.1; --
PDB, 1BXL, 29-OCT-97.
PDB, 1LXL, 21-APR-97.
PDB, 1MAZ, 21-APR-97.
MIM; 600039; --
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226
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189
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148
188
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VARSPLIC
VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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G -> A (IN CAA80661).

Biol. Chem. 271:13258-13265(1996).

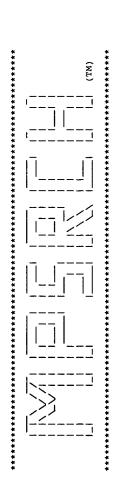
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 SRALVEDLVRYKLCQRSLV--PEPS-GAASCALHSAMRAAGDEFEERFRQAFSEISTQIH 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohta S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 LETNLRDWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGALMTVGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wesselingh S.L., David G.L., Choi S., Veliuona M., Hardwick J.M., Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 96278736.
Shirahwa N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Oh
"An additional form of rat Bcl-x, Bcl-xbeta, generated by an
unspliced RNA, promotes apoptosis in promyeloid cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 900; DB 1; Length 228
Pred. No. 9.34e-181;
36; Mismatches 22; Indels
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LT 4 STANDARD; PRT; 233 AA.
BCLX.RT STANDARD; PRT; 233 AA.
B5356.37, Q62678; P70614; P70613; Q62836; Q64087; Q64128; Q1-0CT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 BH1.
186 BH2.
227 POTENTIAL.
25068 MW; C499D449A585F8A9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (X(L) AND BETA ISOFORMS).
                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
PFAM; PF00452; BC1-2; 1.
                                                                                                                                                                                                                                                                                                                                        EMBL; X82462; CAA57845.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 64.9%;
Local Similarity 66.3%;
hes 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APOPTOSIS REGULATOR BCL-X. BCL2L1 OR BLC2L OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apoptosis; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 1
171 1
207 2
228 AA;
                                                                                                                                                                                                                                                                                                                                                                     P53563; 1AF3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 FASK 228
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                MISSING (IN ISOFORM BCL-X(S)).

PHYDDYGNAAAESKGGRENWENFUGGMYVAGVYLIGSL
FSRK -V RTTPLVCPPLVCLSSVEINOFFWSPGHVVED
IDYSGDIPGLL (IN ISOFORM BCL-X(BETA)).
R -> Q (IN REF. 1).
F -> S (IN REF. 2).
A -> E (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C. -1- SUBCEALULAR LOCATION: MITCHONNEXTAL MEMBERANES AND FEATANCHEARK
ENVELOPE (STIMILARITY).
C. -1- ALTERNATIVE PRODUCTS: THREE ISOFORMS, BCL-X(L) (SHOWN HERE),
BCL-X(S) AND BCL-X(BETA), ARE DERIVED BY ALTERNATIVE SPLICING.
C. -1- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS
SPECIFICALLY EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS
C. OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT
DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
C. DETCTABLE LEVEL OF BCL-X(S).
C. -1- SIMILARITY: CONTAINS A BCL-2 HOWOLOGY DOMAIN 1 (BH1).
C. -1- SIMILARITY: CONTAINS A BCL-2 HOWOLOGY DOMAIN 2 (BH2).
C. -1- SIMILARITY: CONTAINS A BCL-2 HOWOLOGY DOMAIN 3 (BH3).
C. -1- SIMILARITY: CONTAINS A BCL-2 HOWOLOGY DOMAIN 3 (BH3).
C. -1- SIMILARITY: CONTAINS A BCL-2 HOWOLOGY DOMAIN 3 (BH3).
C. -1- SIMILARITY: CONTAINS A BCL-2 HOWOLOGY DOMAIN 4 (BH4).
C. -1- SIMILARITY: BLONGY TO THE BCL-2 FAMILY.
C. -1- SIMILARITY: BLONGS TO THE BCL-2 FAMILY.
                                                                                                                                          Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
"Expression of members of the bol-2 gene family in the immature rat
ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
cell apoptosis is associated with decreased bax and constitutive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
                                                   SEQUENCE FROM N.A. (X(L) AND X(S) ISOFORMS).
STRAIN-SPRAGUE DAWLEX; TISSUE=OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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EMBL; X8237; CAA57887.1; --
EMBL; U10579; AAA19257.1; --
EMBL; U72349; AAB17353.1; --
EMBL; U72349; AAB17352.1; --
EMBL; U72349; AAA17352.1; --
EMBL; S76513; AAA77686.1; --
EMBL; S78284; AAA76670.1; ALT_INIT.
EMBL; S78284; AAC60702.1; --
PDB; 1AR3; 07-JUL-97.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH42; 1.
PROSITE; PS01260; BH42; 1.
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64
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                                                                                                               MEDLINE; 95129487.
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129
180
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64
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CONFLICT
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-i- SUBCELLULAR LOCATION: CYTOPLASMIC.
-i- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,
                                                                                                                                                                                                                                                                                                                                                                                                          61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                   61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G., Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.; "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";
                                                                                                                                                                                                                                                                                        1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y., Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.; Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.; Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain."; DNA Res. 3:321-329(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                              Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                36CA185F5945DFB4 CRC64;
                                                                                                                                                                                                                              Score 1345; DB 1; 1
Pred. No. 1.76e-289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          092843;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
BCL2L2 OR BCLW.
                                                                                                                                                                                                                                                          6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
EMBL; AF030769; AAB86430.1; -. HSSP; P53563; 1AF3.
MGD; MGI:108052; BCL2L2.
PROSITE; P550062; BCL2_FAMILY; 1.
PROSITE; P501080; BH1; 1.
PROSITE; P501260; BH2; 1.
PROSITE; P501260; BH4_1; 1.
PROSITE; P501260; BH4_2; 1.
PROSITE; P500452; BCL22; 1.
                                                                                                                                                    9 29 BH
85 104 BH
136 151 BH
193 AA; 20790 MW;
                                                                                                                                                                                                                            97.08;
                                                                                                                                                                                                                                             95.98;
                                                                                                                                                                                                                                                            185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oncogene 13:665-675(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 GALVTVGAFFASK 192
                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 96358615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 97191544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BCLW_HUMAN
                                                                                                                                      Apoptosis.
                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                    DOMAIN
                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
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Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 193;
SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4). SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 BH4.
104 BH1.
151 BH2.
20774 MW; 3792243A50281761 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 96.8%; Score 1341; DB 1; I
Local Similarity 94.8%; Pred. No. 1.70e-288;
Nes 183; Conservative 8; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARI_XENLA STANDARD; PRT; 228 AA. 091827; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) APOPTOSIS REGULATOR R1 (XR1) (FRAGMENT). Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50062; BCL2_FAMILY; 1. PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1. PROSITE; PS01260; BH4_1; 1. PROSITE; PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                         EMBL; U59747; AAB09055.1; -.
EMBL; D87461; BAA19666.1; -.
HSSP; P53563; IAF3.
MIM; 601931; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00452; Bcl-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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85
136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apoptosis.
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm Run on:

Fri Jun 23 14:18:44 2000; MasPar time 8.06 Seconds 725.519 Million cell updates/sec

Tabular output not generated.

>US-09-155-327B-9 (1-192) from US09155327B.pep 1386 Description: Perfect Score:

1 MPTPASTPDTRALVADFVGY......VTGAVALGALVTVGAFFASK 192 Sequence:

PAM 150 Gap 11 Scoring table:

83857 seqs, 30454973 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot38 1:swissprot

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 45.917; Variance 78.366; scale 0.586

SUMMARIES

|                            | •          | ~          | _         | _         | _          | _          | ~          | ~         | _          |           |            |            |            |                  |                  |           |            |            |                        |            |            |                  |            |
|----------------------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|------------|-----------|------------|------------|------------|------------------|------------------|-----------|------------|------------|------------------------|------------|------------|------------------|------------|
| . No                       | 1.76e-289  | 1.70e-288  | 34e-181   | 13e-114   | 13e-114    | 13e-114    | 09e-113    | 92e-112   | 52e-100    | 1.27e-98  | 1.27e-98   | 72e-98     | 2.78e-96   | 1.42e-26         | 2.28e-26         | 2.45e-25  | 2.45e-25   | 6.32e-25   | 1.01e-24               | .01e-24    | 1.77e-22   | .83e-22          | .78e-18    |
| Pred.                      | 1.7        | 1.7        | 9.3       | 2.1       | 2.1        | 2.1        | 1.0        | 4.9       | 8.5        | 1.2       | 1.2        | 3.7        | 2.7        | 1.4              | 2.2              | 2.4       | 2.4        | 6.3        | 1.0                    | 1.0        | 1.7        | 2.8              | 1.7        |
|                            | BC         | BC         | R1        | BC        | ပ္ထ        | R          | R          | М<br>В    | BC         | В         | ည္က        | R          | R1         | 'AG              | 'AG              | BA        | BA         | BA         | SM                     | BA         | BA         | AG               | ĸ          |
| uc                         | REGULATOR  | REGULATOR  | REGULATOR | REGULATOR | REGULATOR  | REGULATOR  | REGULATOR  | REGULATOR | REGULATOR  | REGULATOR | REGULATOR  | REGULATOR  | REGULATOR  | HOMOLOGOUS ANTAG | DLOGOUS ANTAG    | REGULATOR | REGULATOR  | REGULATOR  | BAX PROTEIN, CYTOPLASM | REGULATOR  | REGULATOR  | DEOGOUS ANTAG    | REGULATOR  |
| Description                | APOPTOSIS  | APOPTOSIS  | APOPTOSIS | APOPTOSIS | APOPTOSIS  | APOPTOSIS  | APOPTOSIS  | APOPTOSIS | APOPTOSIS  | APOPTOSIS | APOPTOSIS  | APOPTOSIS  | APOPTOSIS  | BCL-2 HOM        | BCL-2 HOMOLOGOUS | APOPTOSIS | APOPTOSIS  | APOPTOSIS  | BAX PROTE              | APOPTOSIS  | APOPTOSIS  | BCL-2 HOMOLOGOUS | APOPTOSIS  |
| А                          | BCLW_MOUSE | BCLW_HUMAN | AR1_XENLA | BCLX_RAT  | BCLX_HUMAN | BCLX_MOUSE | BCLX_CHICK | BCLX_PIG  | BCL2_CHICK | BCL2_RAT  | BCL2_HUMAN | BCL2_MOUSE | AR11_XENLA | BAK_HUMAN        | BAK2_HUMAN       | BAXA_RAT  | BAXA_MOUSE | BAXA_BOVIN | BAXD_HUMAN             | BAXA_HUMAN | BAXB_HUMAN | BAK_MOUSE        | NR13_COTJA |
| BB                         | 7          | ٦          | -         | ~         | ч          | -          |            | Н         | -          | <b>~</b>  | Н          | -          | Н          | -1               | Н                | -         | -          | -          | Н                      | Н          | -          | -                | -          |
| å<br>Query<br>Match Length | 193        | 193        | 228       | 233       | 233        | 233        | 229        | 233       | 233        | 236       | 239        | 236        | 204        | 211              | 211              | 192       | 192        | 192        | 143                    | 192        | 218        | 208              | 177        |
| %<br>Query<br>Match        | 97.0       | 96.8       | 6.49      | 44.9      | 44.9       | 44.9       | 44.7       | 44.2      | 40.5       | 40.1      | 40.1       | 40.0       | 39.4       | 17.0             | 16.9             | 16.5      | 16.5       | 16.4       | 16.3                   | 16.3       | 15.5       | 15.4             | 14.1       |
| Score                      | 1345       | 1341       | 006       | 623       | 623        | 623        | 620        | 613       | 561        | 556       | 556        | 554        | 546        | 235              | 234              | 229       | 229        | 227        | 226                    | 226        | 215        | 214              | 195        |
| Result<br>No.              | 1          | 7          | e         | 4         | 'n         | 9          | 7          | æ         | 0          | 10        | 11         | 12         | 13         | 14               | 15               | 16        | 17         | 18         | 19                     | 20         | 21         | 22               | 23         |

| 4.51e-13<br>1.07e-12                             | 3.88e-12<br>1.40e-11<br>9.12e-12   | 4.10e-07               | 6.09e-07               | 5.67e-02               | 1.55e-01               | 5.73e - 01            | 5.73e - 01             | 5.73e-01              | 7.89e-01               | 7.89e-01               | 1.08e+00              | 1.49e+00              | 2.03e+00               | 2.03e+00               | 2.03e+00               | 2.03e+00               |
|--|--|------------------------|------------------------|------------------------|------------------------|-----------------------|------------------------|-----------------------|------------------------|------------------------|-----------------------|-----------------------|------------------------|------------------------|------------------------|------------------------|
| BCL2-RELATED PROTEIN A<br>APOPTOSIS REGULATOR CE | APOPTOSIS REGULATOR CE<br>BCL2-RELATED PROTEIN A<br>INDUCED MYELOID LEHKEM | APOPTOSIS REGULATOR BC | APOPTOSIS REGULATOR BC | NODULATION PROTEIN NOL | GLUCAN 1,3-BETA-GLUCOS | LIGNINASE C PRECURSOR | SIALIDASE PRECURSOR (E | PULLULANASE PRECURSOR | GAG POLYPROTEIN [CONTA | LATENT TRANSFORMING GR | GLUCOSAMINE FRUCTOSE- | NODULATION PROTEIN J. | TRANSALDOLASE (EC 2.2. | TRANSALDOLASE (EC 2.2. | PHOSPHOGLYCERATE KINAS | HYPOTHETICAL 59.4 KD P |
| BFL1_MOUSE<br>CED9_CAEEL                         | CED9_CAEBR<br>BFL1_HUMAN   | EAR_ASFE4              | EAR_ASFB7              | NOLO_RHISN             | EXG_YARLI              | LIGC_TRAVE            | NANH_MICVI             | PULA_THEMA            | GAG_HV2G1              | TGFB_RAT               | GLMS_THETH            | NODJ_BRAJA            | TAL1_MOUSE             | TAL1 HUMAN             | PGKC_LEIME             | YBB9_YEAST             |
| ~~   |  |                        |                        |                        | 7                      | Н                     | Н                      | -                     | Н                      | Н                      | Н                     | Н                     | Н                      | Н                      | Н                      | Н                      |
| 172 280  | 271<br>175<br>350  | 179                    | 179                    | 680                    | 421                    | 372                   | 647                    | 843                   | 522                    | 1712                   | 603                   | 262                   | 337                    | 337                    | 479                    | 520                    |
| 12.0   | 11.5   | 5.6                    | 9.0                    | 7.4                    | 7.1                    | 6.9                   | 6.9                    | 6.9                   | 8.9                    | 6.8                    | 6.7                   | 9.9                   | 9.9                    | 9.9                    | 9.9                    | 9.9                    |
| 167  | 159  | 134                    | 133                    | 102                    | 66                     | 92                    | 92                     | 92                    | 94                     | 94                     | 93                    | 92                    | 91                     | 91                     | 91                     | 91                     |
| 25   | 27<br>27   | 368                    | 31                     | 3 6                    | 34                     | 35                    | 36                     | 37                    | 38                     | 39                     | 40                    | 41                    | 42                     | 43                     | 44                     | 45                     |

## ALIGNMENTS

| RESULT     | 1  |
|------------|--|
| <u>a</u> ; | BCLW_MOUSE STANDARD; PRT; 193 AA.  |
| S E        | יייייייייייייייייייייייייייייייייייייי                                     |
| <u>.</u>   | 33, Creat  |
| <u> </u>   | (Rel. 35, Last   |
| 'n         | 15-JUL-1999 (Rel. 38, Last annotation update)                              |
| E          | APOPTOSIS REGULATOR BCL-W.   |
| SN         | BCL2L2 OR BCLW.  |
| SO         |  |
| 8          | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;              |
| 8          | Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.                   |
| RN         | [1]  |
| RP         | SEQUENCE FROM N.A.   |
| RX         | MEDLINE; 96358615.   |
| RΑ         | Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,          |
| RA         |  |
| RT         | "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";      |
| RL         | Oncogene 13:665-675(1996).   |
| RN         | [2]  |
| RP         | SEQUENCE FROM N.A.   |
| 22         | STRAIN=C57BL/10J;  |
| RX         | MEDLINE: 98160183.   |
| RA         | Ross A.J., Waymire K.G., Moss J.E., Parlow A.F., Skinner M.K.,             |
| RA         | Russell L.D., Macgredor G.R.;  |
| ž          | "Testicular degeneration in Belw-deficient mice.";                         |
| P.         | Nat Genet 18:251-256(1998)   |
| ខ          | - i - FUNCTION - PROMOTES CELL SURVIVAL.                                   |
| 2          | -i- SUBCELLUIAR LOCATION: CYTOPLASMIC.                                     |
| ខ្ល        |  |
| Ü          |  |
| ខ          | AND SALIVARY GLAND.  |
| ပ္ပ        | -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC          |
| ပ္ပ        | FUNCTION.  |
| ပ္ပ        |  |
| ပ္ပ        | SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2                             |
| ပ္ပ        | SIMILARITY:  |
| ပ္ပ        | -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.                               |
| ပ္ပ        |  |
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| ႘          | ee 1   |
| ႘          | license@isb-sib.ch).   |
| ပ္ပ        |  |
| DR         | EMBL; U59746; AAB09056.1;  |
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*Journal Cell (1987) 49:455-463
#title Molecular analysis of mbcl-2: structure and expression of the murine gene homologous to the human gene involved in #cross-references MUID:87187643
#accession B25960
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                                                                                                   *authors Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

#journal Nucleic Acids Res. (1992) 20:4187-4192

#title Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
#cross-references MUID:92375724
#accession D37332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 GAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 503; DB 2; Length 206;
Pred. No. 4.22e-76;
30; Mismatches 29; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVMSB1 #type complete transforming protein bcl-2-beta - mouse #formal_name Mus musculus #common_name house mouse 31-bec-1988 #sequence_revision 31-bec-1988 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                 D37332 *type complete transforming protein (bcl-2-beta) - human *forming protein (bcl-2-beta) - human #formal_name Homo sapiens *common_name man 03.Mar-1993 *sequence_revision 03-Mar-1993 *text_change 23.Peb-1997
                                                                                                                                                                                                                                                                                                           preliminary; nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                              #superfamily bcl transforming protein
mitochondrion
#length 206 #molecular-weight 22440 #checksum 5581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 GVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGW 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #superfamily bol transforming protein
alternative splicing; transforming protein
#length 199 #molecular-weight 22299 #checksum 7397
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Pred. No. 1.09e-75;
29; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                          1-206 ##label EGU
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Best Local Similarity 48.7%;
Matches 56; Conservative
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Best Local Similarity 48.7%;
Matches 57; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          ##residues
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Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler,
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PID:g510899
                                                                                                                                                                                                                             Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.;
                                                                                                                                                                                                                                                                  Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 ASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFHDGVNWGRIVA 138
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bol-x, a bol-2-related gene that functions as a dominant
regulator of apoptotic cell death.
noes MUID:93364977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #formal_name Gallus gallus #common_name chicken
03-May-1994 #sequence_revision 03-May-1994 #text_change
16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #formal_name Homo sapiens #common_name man
21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #superfamily_bcl transforming protein
#length 190 #molecular-weight 21467 #checksum 5509
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#length 227 #molecular-weight 25290 #checksum 864
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Pred. No. 1.09e-82;
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apoptosis regulator bcl-x isoform - human
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Pred. No. 1.09e-82;
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##molecule_type DNA
1-190 ##label BOI
1-001110; GB:
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llarity 52.9%;
Conservative
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58.9%;
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#journal Blochim. Blophys. Acta (1992) 1132:109-113
#title Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue of the Bcl-2 oncoprotein.
#cross-references MUID:92379084
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                                                                                                                                                                                                                                                                                                                                                                                        #superfamily bcl transforming protein alternative splicing; mitochondrion; transforming protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 VATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 GCAAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTATGRFVAVVEELFRDGVNWV 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transforming protein (Bcl-2) homolog - chicken formal_name Gallus gallus *common_name chicken 13-Jan-1995 *sequence_revision 13-Jan-1995 *text_change 16-Jul-1999
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                                                                             eliminary; nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transmembrane protein
#length 236 #molecular-weight 26524 #checksum 6709
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                                                                                                                                                                                                                    1-33,'E',34-220,'AL',223-236 ##label EGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 540; DB 2; Length 232
Pred. No. 1.01e-83;
37; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 VELYGP-SM---RPLFDFSWLSLKTLLSLP-WVGACITLGAYLGHK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 TALYGDGALEDARRIREGNW-AVSTVVTGAVALGALVTVGAFFASK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :: | | :: | | :: | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 |
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                                                                             preliminary;
#cross-references MUID:92375724
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ilarity 42.8%;
Conservative
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Best Local Similarity 44.3%;
Matches 70; Conservative
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                                                                                                                                                                            ##molecule_type DNA
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Best Local Similarity
Matches 71; Conserv
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                                                                                                                                         #authors Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
#journal Endocrinology (1995) 136:232-241
#title Expression of members of the bcl-2 gene family in the immarture rat ovary: equine choriong gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 RDGVNWGRIVAFFEFGGVMCVESVNREMYPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 551; DB 2; Length 236;
Pred. No. 5.40e-86;
45; Mismatches 43; Indels 6; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BCL-2 - rat (fragment)
#formal_name Rattus norvegicus #common_name Norway rat
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene bcl-2 protein - rat
#formal_name Rattus norvegicus #common_name Norway rat
29-May-1998 #sequence_revision 29-May-1998 #text_change
16-Jul-1999
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Cloning and sequencing of a CDNA encoding the rat Bcl-2
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#length 236 #molecular-weight 26550 #checksum 8001
                                                                                                                                                                                                                                                                                                                                                              ##cross-references EMBL:U34964; NID:g1004378; PIDN:AAA77687.1;
PID:g1004379
                                                                                                                                                                                                                                                                                                           preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 VELYGP-SM---RPLFDFSWQSLKTLLSLAL-VGACITLGAYLGHK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #superfamily bcl transforming protein
#length 236 #checksum 9134
                      #type fragment
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Best Local Similarity 43.4%;
Matches 72; Conservative
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Best Local Similarity 42.8%;
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                            ##molecule_type mRNA
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Cell (1987) 49:455-463
Molecular analysis of mbcl-2: structure and expression of the
murine gene homologous to the human gene involved in
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Nucleic Acids Res. (1992) 20.4187-4192
Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
neuronal organs in adult and embryo.
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##cross-references GB:L31532; GB:M16506; NID:g468336; PIDN:AAA37282.1;
PID:g387109
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136 RDGVNWGRIVAFFEFGGVMCVGSVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
                                  88 QGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDMIVAXLETRLADWIHSSGGWADF 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. (1994) 153:4388-4398
Cloning and molecular characterization of mouse bcl-x in
and T lymphocytes.
                                                                                                                                                                                                                                                   149057 #type complete
bcl-x transmembrane deleted - mouse
#formal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transforming protein bcl-2-alpha - mouse
#formal_name Mus musculus #common_name house mouse
31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bcl.x-long
#superfamily bcl transforming protein
#length 214 #molecular-weight 23900 #checksum 9730
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##cross-references EMBL:U10102; NID:9506649; PIDN:AAA82174.1;
PID:9506650
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39.1%; Score 542; DB 2; Length 214
Local Similarity 57.9%; Pred. No. 3.92e-84;
les 62; Conservative 24; Mismatches 21; Indels
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                                                                                                                                                    | | | | :: | | : : | :: | :: | | : : | | 148 TALYGDGALEDARRLREGNW-AVSTVVTGAVALGALVTVGAFFASK 192
                                                                                                                     196 VELYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK
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#cross-references MUID:87187643
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##residues 1-23
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#journal Nucleic Acids Res. (1992) 20:4187-4192
#title Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
neuronal organs in adult and embryo.
                                                                                                                                                                                                                                                                                                                                                                                                                                       #superfamily bel transforming protein
mitochondrion; transforming protein; transmembrane protein
#length 233 #molecular-weight 25687 #checksum 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 PAPAAAPAAVAAGASSHHRPEPPGSAAASEVPPAEGLRPAPPGVHLALRQAGDEFSRRY 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 QRDFAQMSGQLHLTPFTAHGRFVAVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSP 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PIPASIPDIRALVADEVGYRLROKGYVCGAG--PGEG-PAADP-LHQAMRAAGDEFEIRF 57
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                                                                                     A37332 #type complete
transforming protein (bol-2-alpha) - chicken
#formal_name Gallus gallus #common_name chicken
03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
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Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5214-5218
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40.5%; Score 561; DB 2; Length 233; Best Local Similarity 40.5%; Pred. No. 4.59e-88; Matches 79; Conservative 47; Mismatches 61; Indels
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##cross-references EMBL:D11381
                                                                                                                                                                         A37332; S35453
                                                                                                                                                          23-Feb-1997
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blocks apoptosis in hematopoietic cells
#superfamily bcl transforming protein
alternative splicing; B-cell lymphoma; follicular lymphoma;
proto-oncogene; transforming protein; transmembrane protein
#length 239 #molecular-weight 26266 #checksum 8323
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#title Cloning and structural analysis of cDNAs for bc1-2 and a hybrid bc1-2/immunoglobulin transcript resulting from the t (14:18) translocation.
#cross-references MUID:87002488
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##residues 1-58,'T',60-116,'R',118-239 ##label CLE
##cross-references GB:M14745; NID:g179370; PIDN:AAA35591.1; PID:g179371
                                                                                                                                                                                                                                                                                                      Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsmeyer, S.J.

EMBO J. (1988) 7:123-131
Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2--19 fusion gene in lymphoma.
                  protein products
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#authors Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.;
#yright, J.J.; Bakhshi, A.
#yright, J.J.; Bakhshi, A.
#journal Oncogene Res. (1988) 2:263-275
#title Consequences of the t(14;18) chromosomal translocation in follicular lymphoma: deregulated expression of a chimeric and mutated BCL-2 gene.
#cross-references MUID:88217344
#title Analysis of the structure, transcripts, and protein product
    of bcl-2, the gene involved in human follicular lymphoma.
#cross-references MUID:86259760
#accession A29409
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40.1%; Score 556; DB 1; Length 239;
Best Local Similarity 43.3%; Pred. No. 4.98e-87;
Matches 71; Conservative 46; Mismatches 41; Indels
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##cross-references GDB:119031; OMIM:151430
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BCL-X protein rat #formal_name Norway rat #formal_name Rattus norvegicus #common_name Norway rat 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 16-0ul-1999
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##residues 1-233 ##label MIC
##cross-references EMBL:X82537; NID:g607176; PIDN:CAA57886.1;
##cross-references PID:g607177
                                                                                                                                                                                                               Michaelidis, T.M.
submitted to the EMBL Data Library, November 1994
S51761
                                                                              #type complete
161 RLREG-N-WAVSTV-VTGAVALGAL 182
                                                                                                                                                                                                                                                                        preliminary
                                                                                                                                                                          S51761; S51762
                                                                                                                                                                                                                                                                                                                                                                                                                #submission
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                                                                                                                                                                                            REFERENCE
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                                                                                            TITLE
ORGANISM
                                                         RESULT
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##residues 1-125,189-233 ##label MI2 ##cross-references EMBL:X82537; NID:g607176; PIDN:CAA57887.1; PID:g607178 Michaelidis, T.M. submitted to the EMBL Data Library, November 1994 preliminary ##molecule\_type DNA S51762 ##status #accession

125/3 #superfamily bcl transforming protein #length 233 #molecular-weight 26130 #checksum 6378 #introns CLASSIFICATION GENETICS SUMMARY

3; Gaps Length 233; Indels Score 623; DB 2; Le Pred. No. 5.74e-101; 34; Mismatches 32; Query Match
Best Local Similarity 52.4%;
Matches 76; Conservative

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145 SFGGALCVESYDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 204 ò g

205 KGQERFNRWFLTGMTVAGVVLLGSL 229 셤

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B47537 #type complete
apoptosis regulator bcl-xL - human
bcl-2-related protein
apoptosis regulator bcl-xS
aformal\_name Homo saplens #common\_name man
16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change ALTERNATE\_NAMES m CONTAINS ORGANISM RESULT ENTRY

B47537; C47537

ACCESSIONS

Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson, #authors REFERENCE

#journal Cell (1993) 74:597-608 #title bcl.x, a bcl.2-related gene that functions as a dominant regulator apoptotic cell death. #cross-references MUID:93364977 B47537 \*accession

##status

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##cross-references GB:L20121; NID:g510900; PIDN:CAA80661.1; PID:g510901 1-233 ##label BOI GB/EMBL/DDBJ ##molecule\_type mRNA ##residues

nucleic acid sequence not shown; translated from

##residues 1-69, 'G',71-125,189-233 ##label BO2 ##cross-references GB:L20122; NID:g623236; PIDN:CAA80662.1; PID:g623237 ë, #product apoptosis regulator bcl-xL #status predicted 85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144 145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204 Gaps .; ; nucleic acid sequence not shown; translated Query Match 44.9%; Score 623; DB 2; Length 233; Best Local Similarity 52.4%; Pred. No. 5.74e-101; Matches 76; Conservative 34; Mismatches 30: Tradi-#superfamily bcl transforming protein alternative splicing; apoptosis 205 KGQERFNRWFLTGMTVAGVVLLGSL 229 GB/EMBL/DDBJ ##cross-references GDB:228079 #label MAT ##molecule\_type mRNA ##residues 1-69, C47537 1-125,189-233 CLASSIFICATION ##status #accession GENETICS KEYWORDS #gene 1 - 233FEATURE SUMMARY 셤 ò g g ò

#authors Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
#journal Endocrinology (1995) 136:232-241
#title Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels. BCL-X-Long - rat
#formal\_name Rattus norvegicus #common\_name Norway rat
26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change
16-Jul-1999 preliminary; translated from GB/EMBL/DDBJ #type complete 153295 167431 I67431 ##status #accession ACCESSIONS REFERENCE ORGANISM RESULT TITLE DATE

#superfamily bcl transforming protein #length 233 #molecular-weight 26122 #checksum 8310 ##molecule\_rype mous:
##residues 1-233 ##label RES
##cross-references EMBL:U34963; NID:g1004376; PIDN:AAA77686.1;
##cross-references PID:g1004377 ##molecule\_type mRNA CLASSIFICATION SUMMARY

3; Gaps Query Match 42.2%; Score 585; DB 2; Length 233; Best Local Similarity 49.7%; Pred. No. 4.78e-93; Matches 72; Conservative 35; Mismatches 35; Indels

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85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTVYQSFEQVVNELFRDGVNWGRIVASS 144 셤 ă

145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNTAPESR 204 셤

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205 KGQERFNRWFLTGMTVAGVVLLGSL 229 g

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Fri Jun 23 14:18:10 2000; MasPar time 12.63 Seconds 716.856 Million cell updates/sec MPsrch\_pp Run on:

Tabular output not generated.

>US-09-155-327B-9
(1-192) from US09155327B.pep
1386
1 MPTPASTPDTRALVADFVGY......VTGAVALGALVTVGAFFASK 192

Description: Perfect Score: Sequence:

PAM 150 Gap 11

Scoring table:

142080 seqs, 47172406 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Mean 44.905; Variance 86.927; scale 0.517 Statistics:

pir63 1:pir1 2:pir2 3:pir3 4:pir4

Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|               |       | ď              |                          |    |        |                       |           |
|---------------|-------|----------------|--------------------------|----|--------|-----------------------|-----------|
| Result<br>No. | Score | Query<br>Match | Query<br>Match Length DB | DB | ID     | Description           | Pred. No. |
| 1             | 623   | 44.9           | 233                      | 7  | I49056 | bcl-x long - mouse    | 5.74e-101 |
| 7             | 623   | 44.9           | 233                      | 7  | S51761 | BCL-X protein - rat   | 5.74e-101 |
| e             | 623   | 44.9           | 233                      | 7  | B47537 | apoptosis regulator b | 5.74e-101 |
| 4             | 585   | 42.2           | 233                      | ~  | 167431 | BCL-X-Long - rat      | 4.78e-93  |
| S             | 561   | 40.5           | 233                      | 7  | A37332 | transforming protein  | 4.59e-88  |
| 9             | 556   | 40.1           | 239                      | Н  | TVHUA1 | transforming protein  | 4.98e-87  |
| 7             | 551   | 39.8           | 236                      | 7  | 167432 | BCL-2 - rat (fragment | 5.40e-86  |
| 8             | 549   | 39.6           | 236                      | ~  | 153744 | gene bcl-2 protein -  | 1.40e-85  |
| 6             | 542   | 39.1           | 214                      | ~  | 149057 | bcl-x transmembrane d | 3.92e-84  |
| 10            | 542   | 39.1           | 236                      | -  | TVMSA1 | transforming protein  | 3.92e-84  |
| 11            | 540   | 39.0           | 232                      | 7  | S24390 | transforming protein  | 1.01e-83  |
| 12            | 535   | 38.6           | 190                      | 7  | A47537 | apoptosis regulator b | 1.09e-82  |
| 13            | 535   | 38.6           | 227                      | 7  | JE0203 | apoptosis regulator b | 1.09e-82  |
| 14            | 503   | 36.3           | 206                      | ~  | D37332 | transforming protein  | 4.22e-76  |
| 15            | 501   | 36.1           | 199                      | -  | TVMSB1 | transforming protein  | 1.09e-75  |
| 16            | 495   | 35.7           | 216                      | 7  | B37332 | transforming protein  | 1.85e-74  |
| 17            | 491   | 35.4           | 205                      | 7  | TVHUB1 | transforming protein  | 1.22e-73  |
| 18            | 404   | 29.1           | 154                      | 7  | 158194 | qene bcl-2 protein -  | 5.41e-56  |
| 19            | 235   | 17.0           | 211                      | 7  | S58873 | Bak protein - human   | 2.90e-23  |
| 20            | 234   | 16.9           | 211                      | ~  | S58875 | cdn-2 protein - human | 4.43e-23  |
| 21            | 233   | 16.8           | 192                      | ~  | D47538 | bcl-2-associated prot | 6.76e-23  |
| 22            | 226   | 16.3           | 143                      | N  | 138921 | bcl-2-associated prot | 1.29e-21  |
| 23            | 226   | 16.3           | 192                      | ~  | A47538 | bcl-2-associated prot | 1.29e-21  |

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205 KGQERFNRWFLTGMTVAGVVLLGSL 229 :: | | | | :: | | | | | | |

| 1.96e-21<br>1.26e-19<br>7.78e-18   | 4.55e-16<br>2.92e-11<br>6.31e-11<br>6.23e-10   | 4.27e-10<br>1.84e-01<br>4.58e-01<br>1.12e+00  | 1.12e+00<br>2.01e+00<br>2.01e+00<br>2.01e+00<br>2.69e+00   | 2.69e+00<br>2.69e+00<br>2.69e+00<br>2.69e+00<br>3.58e+00   |
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| bcl-2-associated prot<br>bcl-2-associated prot<br>bcl-x short - mouse<br>dene bcl-xshort prote | WR-13 protein - quail<br>hemopoletic-specific<br>apoptosis suppressor<br>BC1-2 related - human | BCL2 homolog MCL1 - h<br>hypothetical protein<br>angiotensin-convertin<br>probable transitional | probable polyketide s<br>lignin peroxidase (EC<br>exo-alpha-sialidase (<br>pullulanase - Thermot<br>hypothetical protein | gāg polyprotein - hum<br>cell division control<br>masking protein precu<br>fatty-acid synthase (<br>hypothetical protein |
| 153295<br>B47538<br>149055<br>T67435   | S54778<br>I49449<br>A53189<br>I39055   | A47476<br>T03168<br>JC5374<br>B71196  | T03224<br>S32581<br>A45244<br>H72204<br>C70667   | FOLJGG<br>F75154<br>A38261<br>S20473<br>E70529   |
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| 133<br>218<br>170  | 177<br>172<br>280<br>175   | 350<br>168<br>630<br>798  | 1937<br>372<br>647<br>843<br>494   | 522<br>795<br>1712<br>3104<br>657  |
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| 16.<br>15.   | 14.1<br>12.0<br>11.9<br>11.5   | 11.5<br>7.4<br>7.2<br>7.0   | 7.0000   | 6.886.7  |
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## ALIGNMENTS

| 149056 #type complete bcl.* long - mouse #formal_name Mus musculus #common_name house mouse 02-0ul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999 149056; 552866 | #authors Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W. #journal J. Immunol. (1994) 153:4388-4398 #fitle Cloning and molecular characterization of mouse bcl-x in B #cross-references MUID:9505269. | design 149056 ##status preliminary; translated from GB/EMBL/DDBJ ##status preliminary; translated from GB/EMBL/DDBJ ##molecule_type mRNA ##residues 1-233 ##label RES ##cross-references EMBL:U10101; NID:9506647; PIDN:AAA82173.1; | Kamesaki<br>Submitte<br>IL-5 inh<br>cell 1<br>S52866<br>e_type mRN<br>s 1-2   | ASSIFICATION #superfamily bcl transforming protein MMARY #length 233 #molecular-weight 26132 #checksum 5739 Query Match 44.9%; Score 63; DB 2; Length 233; Best Local Similarity 52.4%; Pred. No. 5.74e-101; Matches 76; Conservative 34; Mismatches 32; Indels 3; Gaps 3; | 85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144 : |
|--|---|---|---|--|---|
| RESULT 1 ENTRY TITLE ORGANISM DATE ACCESSIONS  | # Enthors<br># # authors<br># fitle<br># cross - refer  | #accession<br>#accession<br>##status<br>##molecule<br>##residues<br>##cross-re  | KEFEKULE<br>#authors<br>#submission<br>#description<br>#accession<br>##status<br>##moleoule<br>##residues<br>##residues | CLASSIFICATION SUMMARY Query Match Best Local S: Matches 70  | Db 85 AVKQi<br>::  <br>Qy 41 PLHQi                                    |

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        Query Match
12.1%; Score 168; DB 13; Length 211;
Best Local Similarity 22.7%; Pred. No. 1.23e-12;
Matches 30; Conservative 31; Mismatches 70; Indels 1; Gaps 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MYELOID CELL LERKEMIA PROTEIN MCL-1 (FRAGMENT).
Gallus gallus (Chicken).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 -PNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTA 149
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                                                                                                                                                                                                                                                                                                                                                                                                                     72 PGSAQQRFTQVSDELFQGG-PNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDMIVAXL 130
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                                                                                                                                                                                                                                                                               160 EIISRY-LREQATGSKDAKPLGEAGAAGRRALETLRRVGDGVQRNHETAFQGMLRKLDIK 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEE R.M., GILLET G., BURNSIDE J., THOWAS S.J., NEIMAN P.; "Role of Nr13 in regulation of programmed cell death in the bursa of
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                           9
                                                                                                                                                               Query Match 12.6%; Score 175; DB 11; Length 330; Best Local Similarity 24.5%; Pred. No. 6.35e-14; Matches 37; Conservative 33; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AF115380; AAD13295.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFER L., BURNSIDE J.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF120210; AAD31644.1; -.
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077738 PRELIMINARY; PRT; 80 AA.
077738; 017738; 01.NOV-1998 (TEMBLrel. 08, Last sequence update)
01.NOV-1999 (TEMBLrel. 12, Last annotation update)
BAK PROTEIN (FRAGMENT).
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PROSITE; PS01080; BH1; 1.
SEQUENCE 330 AA; 35195 WW; CC87F2E0 CRC32;
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                                                                                                 **BARTLING B., HOFFMANN J., HOLTZ J., SCHULZ R., HEUSCH G., DARMER D.; "Expression of apoptosis-associated genes in hibernating and stunned myocardium of pig.";
submitted (JAN.1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ001204; CAA04598.1;
HSSP; Q16611, IBX.
PROSITE: PS01259; BH3; 1.
PPROSITE: PS01259; BH3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NUV-1999 (TrEMBLrel. 12, Last annotation update)
B-CELL LEDKEMIA/LYMPHOMA 2 RELATED PROTEIN ALC (Al-C PROTEIN).
BCL2ALC OR ALC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-129/SV; TISSUB-LIVER; HATAKEYAMA S., HAMASAKI A., NEGISHI I., LOH D.Y., SENDO F., MAKAYAMA K., NKAYAMA K., I.; II.; Immunol. 0:0-0(1998).
EMBL; U23779; AAB97955.1; -.
                                                                                                                                                                                                                                                                                                                                                                                            Score 144; DB 6; Length 80;
Pred. No. 2.28e-08;
15; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 GDDINRRYDSEFQAMLQHLQPTAENAYEYFTKIASSLFESGINWGRVV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 DFHVESIDTTRIFNQVMEKEFEDGIINWGRIVTIFAFGGVL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 120; DB 11;
Pred. No. 2.21e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1278327; Bcl2alc.
PROSITE; PS01080; BHL; 1.
PFAM; PF00452; Bcl-2; 1.
SEQUENCE 128 AA; 14763 MW; DF4F2653 CRC32;
                                                                                                                                                                                                                                                                                                                                                     80 AA; 8818 MW; 973BE2D0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 8.7%;
Local Similarity 38.1%;
les 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 35.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                          SEQUENCE FROM N.A.
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80
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SEQUENCE
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055178
055178;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 SPTDKELVAQAKALGREYVHARLLRAGLSWSAPERASPAPGG-RLAEVCTVLLRLGITWG 79
                                                                                                                                                      :|: | :| |: | |: || 36 GPAADPLHQAMRAAGDEF-ETRFRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWG 94
                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
B-CELL LEGKEMIA/LYMPHOMA 2 RELATED PROTEIN AlB (Al-B PROTEIN).
                                                                                                                                                                                                                       80 KVVSLYSVAAGLAVDCVRQAQPAMVHALVDCLGEFVRKTLATWLRRRGGWTD 131
                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
B-CELL LEUKEMIA/LYMPHOMA 2 RELATED PROTEIN AID (A1-D PROTEIN)
BCL2AID OR AID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                      Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=129/SV; TISSUE=LIVER;
HATAKEYAMA S., HAMASAKI A., NEGISHI I., LOH D.Y., SENDO F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=129/SV; TISSUE=LIVER;
HATAKEVAMA S., HAMASKI A., NEGISHI I., LOH D.Y., SENDO F.,
HATAKIYAMA K., NAXAMA K.-I.;
Int. Immunol. 0:0-0(1998).
EMBL; U23781; AAB97956.1; -.
EMBL; U23780; AAB97956.1; -.
                                                                   Ouery Match 12.7%; Score 176; DB 11; Length 17
Best Local Similarity 25.0%; Pred. No. 4.14e-14;
Matches 28; Conservative 35; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF051093; AAC61928.1; ... SEQUENCE 170 AA; 18729 MW; 79B4BBE6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 6.35e-14;
20; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00452; BC1-2; 1.
SEQUENCE 172 AA; 20048 MW; FA16DF6C CRC32;
                                                                                                                                                                                                                                                                                                        PRT; 172 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 172 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 12.6%; Score 175;
Local Similarity 33.7%; Pred. No. 6
nes 29; Conservative 20; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 QVQDWIVAYLETRLADWIHSSGGWAD 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 QVSSFVAEFIINNTGEWIRRNGGWED 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAKAYAMA K., NAKAYAMA K.-I.;
Int. Immunol. 0:0-0(1998).
EMBL; U23778; AAB97954.1; -.
EMBL; U23777; AAB97954.1; -OINED.
MGD; MGI:1278326; BG12alb.
PROSITE; PS01080; BH1; 1.
                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         BCL2A1B OR A1B
                                                                                                                                                                                                                                                                                     ILT 9
055177
055177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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055179
055179;
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                             58 DFHVESIDTARIIFNQVMEKEFEDGIINWGRIVTIFAFGGVL-LKKLPQEQIALDVGAYK 116
                                                                                                                                                                 87 GRIMTIFTFGGLL-TKKLQEHGVQLTGEEKEKISYFITEYIINNKAAWIDANGGWENGFL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEE R.M., GILLET G., BURNSIDE J., THOMAS S.J., NEIMAN P.; "Role of Nr13 in regulation of programmed cell death in the bursa of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 12.6%; Score 174; DB 13; Length 174;
Best Local Similarity 24.4%; Pred. No. 9.71e-14;
Matches 30; Conservative 33; Mismatches 52; Indels 8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 GPAQTRVAHVLRNIASSLQDQTEEALRPFLDRIDITSVDVAKRIFNGVMEEKFADGNINW 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                    Length 172;
                                                                                Score 174; DB 11; Length 172
Pred. No. 9.71e-14;
20; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.
SOFER L., BURNSIDE J.;
SUDMITTED (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF120211; AAD31645.1; -
SEQUENCE 174 AA; 20095 MW; 70F5FDAA CRC32;
                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
LEO C.P., HSU S.Y., HSUEH A.J.W.;
"Sequence of rat Mcl-1, a Bcl-2-related gene.";
MGD; MGI:1278325; Bcl2ald.
PROSITE; PS01080; BHI; 1.
PRAM; PPF0452; Bcl-2; 1.
SEQUENCE 172 AA; 20048 MW; 1B340DDD CRC32;
                                                                                                                                                                                                                                                                                                                  174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330 AA
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01-MAY-1999 (TrEMBLrel. 10, Last sequ
01-NOV-1999 (TrEMBLrel. 12, Last anno
                                                                                                                                                                                                                                 121 QVQDWIVAYLETRLADWIHSSGGWAD 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                              117 OVSSFVAEFIMNNTGEWIRRNGGWED 142
                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes Dev. 13:718-728(1999).
                                                                               Query Match 12.6%;
Best Local Similarity 33.7%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 99190706.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fabricius."
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                                                                                                                                                                                                                                                                                                                                Q9W6F2;
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09W6F2
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Q9Z1P3
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AC 099
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"Bok is a pro-apoptotic Bcl-2 protein with restricted expression in reproductive tissues and heterodimerizes with selective anti-apoptotic Bcl-2 family members.";

Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 GDEFETRFRIT-FSDLAAQLHVT-PG-SA-QQRFTQVSDELFQGGPNWGRLVAFFVFGAA 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INCHARA N., EKHTERAE D., GARCIA I., CARRIO R., MERRY A., CHEN S., NUNEZ G.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF0277954, AAB87418.1;
EMBL; AF027777; AAC35582.1;
PFAM; PF00452; BCI-2; 1.;
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5,
                                                                                                                                                                                                                                                                             8; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat), and Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                 Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                         85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQDSFVDLY 132
                                                                                                                                                                                                                                                                                                                                                                         HSU S.Y., HSUEH A.J.W.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
HE X.J., JIN K.L., GRAHAM S.H., SIMON R.P.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF136230; AAD33683.1; -.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4.1; 1.
SEQUENCE 170 AA; 19031 MW; 8B29C9C1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY, TESTIS, UTERUS; MEDLINE; 98024143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY, TESTIS, UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.1%; Score 182; DB 11; 27.7%; Pred. No. 3.16e-15;
                                                                                                                                                                                                                 Score 207; DB 11;
Pred. No. 5.41e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23456 MW; 29761D17 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         331 AA.
                                                                                                                                                                                                                                                                             11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 213 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCL-2-RELATED OVARIAN KILLER PROTEIN.
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                                                                                                                                                                                                                    / Match
Local Similarity 58.3%;
hes 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 27.7%;
Matches 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-MOUSE;
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HSU S.Y., KAIPIA A., MCGEE E., LOMELI M., HSUEH A.J.; Bot is a pro-apoptotic Bcl-2 protein with restricted expression in reproductive tissues and heterodimerizes with selective anti-apoptotic Bcl-2 family members.";
                                                                                                                                                                                                                                                               CHAO J.R., WANG J.M., LEE S.F., PENG H.W., LIN Y.H., CHOU C.H.,
LI J.C., HUDANG H.M., CHOU C.K., KUO M.L., YEN J.J.Y., YANG-YEN H.F.;
"mcl-1 is an immediate-early gene activated by the granulocyte-
macrophage colony-stimulating factor (GM-CSF) signaling pathway and is
one component of the GM-CSF viability response.";
Mol. Cell. Biol. 18:4883-4898(1998).
EMBL; ARG31990.1; -.
EMBL; ARG31886; AAC27929.1; -.
HSSP; Q07817; IMAZ.
MGD; MGI:101769; MGI.
MGD; MGI:101769; MGI.
PROSITE; PS01080; BHI: 1.
SEQUENCE 331 AA; 35217 MW; 3103C5FE CRC32;
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TISSUE-OVARY, UTERUS;
HSU S.Y., HSUEH A.J.W.;
A splicing variant of the Bcl-2 member Bok with a truncated BH3
domain induces apoptosis without dimerization with anti-apoptotic Bcl-
                                                                      SEQUENCE FROM N.A.
MEDLINE; 98322120.
OKITA H., UMEZAWA A., SUZUKI A., HATA J.;
"Up-regulated expression of murine Mcil/EAT, a bcl-2 related gene, in the early stage of differentiation of murine embryonal carcinoma cells and embryonic stem cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GEAGAAGRRALETLRRVGDGVQRNHETAFQGMLRKLDIKNEGDVKSFSRVMVHVFKDGVT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 NWGRLVAFFVFGAALCAESVNK-EMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTAL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 NWGRIVTLISFGA-FVAKHLKSVNQESFIEPLAETITDVLVRTKRDWLVKQRGWDGFVEF 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 GE-GPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGG-P 91
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 177; DB 11; Length 33
Pred. No. 2.70e-14;
30; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
BCL-2-RELATED OVARIAN KILLER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).
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                                                                                                                                                                                Biochim. Biophys. Acta 1398:335-341(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 25.2%;
nes 33; Conservative
                                                                                                                                                                                                                    SEQUENCE OF 1-65 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
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TISSUE=OVARY, UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 FHVQDLEGGIR 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 YGDGALEDARR 161
                                                                                                                                                                                                                                                         MEDLINE; 98336293.
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088857
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229 AA; 25099 MW; E82B3DFB CRC32;
  SEQUENCE
                                           Query Match
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035843
035843;
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Q9WUI5
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                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 SFGCALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 204
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                                                                                                                                                                                                                                                                                                                                                                                             YANG X.-F., WEBER G.F., CANTOR H.;
"A novel Bcl-x isoform connected to the T cell receptor regulates apoptosis in T cells.";
Immunity 7:629-639(1997).
EMBL; U51218; AAC53459.1; -.
HSSP; P53563; lAF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 3
002718 PRELIMINARY; PRT; 229 AA.
002718; CTEMBLrel. 04, Created)
01-JUL-1997 (TTEMBLrel. 04, Last sequence update)
01-JUL-1999 (TTEMBLrel. 12, Last annotation update)
01-NOV-1999 (TTEMBLrel. 12, Last annotation update)
BCL-2 (FRAGMENT).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Peccoa; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 638; DB 11; Length 233;
Pred. No. 2.64e-113;
34; Mismatches 31; Indels
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STRAIN-HOLSTEIN; TISSUE=THYMUS;
STRAIN-HOLSTEIN; TISSUE=THYMUS;
REYES R.A., COCKERELG G.L.;
RENEL; U92434; AAB53319.1; -. EMBL/GenBank/DDBJ databases.
EMBL; U92434; AAB5319.1; -. FSBL PSSTG; PS01080; BH1; 1.
PROSTIE; PS01080; BH2; 1.
PROSTIE; PS01259; BH3; 1.
PROSTIE; PS01259; BH3; 1.
PROSTIE; PS01250; BH3; 1.
PROSTIE; PS01260; BH4_1; 1.
PROSTIE; PS01260; BH3; 1.
PROSTIE; PS01260; BH3; 1.
NON_TER 229 229
                                                                                                                              Created)
Last sequence update)
Last annotation update)
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PROSITE; PS01080; BH1; 1.
PROSITE; PS01289; BH3; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4!; 1.
PROSITE; PS0452; BG1-2: 1.
SEQUENCE 233 AA; 26033 MW; A4A14278 CRC32;
                                                                                     233 AA
                                                                                       PRT;
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161 RLREG-N-WAVSTV-VTGAVALGAL 182
                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
STRAIN-B6/CBA; TISSUE-THYMUS;
MEDLINE; 98051053.
                                                                                                                              (TrEMBLrel. 05, (TrEMBLrel. 05, 1 (TrEMBLrel. 12, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 46.0%;
Local Similarity 53.1%;
hes 77; Conservative
                                                                                       PRELIMINARY;
  180 GALVTVGAFFASK 192
                                                                                                                                                                                                 BCL2-LIKE (BCL-XL).
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                                                                                                                                01-JAN-1998
01-JAN-1998
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035844;
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                                                                                                                                                                                                                                        6; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-B6/CBA; TISSUE-THYMUS;
MEDLINE; 98051053.
MACK X.-F., WEBER G.F., CANTOR H.;
"A novel Bel.x lsoform connected to the T cell receptor regulates apoptosis in T cells:";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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  Length 229;
Match 40.4%; Score 560; DB 6; Length 229; Local Similarity 42.7%; Pred. No. 1.15e-95; Local 70; Conservative 48; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWA 145
                                                                                                                                                                                                                                                                                                                                           191 LYGP-SM---RPLFDFSWLSLKALLSLAL-VGACITLGAYLGHK 229
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 AA
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01-NOV-1999 (TrEMBLrel. 12, Last sequ
01-NOV-1999 (TrEMBLrel. 12, Last anno
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EMBL: U5127; AAC53458.1; --
HSSP: P5363; 1AF3.
MCD: MCI: 88139; Bc121.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01259; BH3; 1.
PRAM: PF00452; BC1-2; 1.
SEQUENCE 235 AA; 26122 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-NOV-1999 (TrEMBLrel. 12, BCL2-LIKE (BCL-X-GAMMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCL-X SHORT.
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| ****                                    | (TM) |
|---|------|
| ******                                  |      |
| ******                                  | [    |
| *****                                   |      |
| ****                                    |      |
| *************************************** |      |
| ******                                  |      |
| *****                                   | [    |

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Fri Jun 23 14:19:13 2000; MasPar time 19.74 Seconds 674.404 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-155-327B-9 (1-192) from US09155327B.pep 1386

Description: Perfect Score: Sequence:

1 MPTPASTPDTRALVADFVGY......VTGAVALGALVTVGAFFASK 192

PAM 150 Gap 11 Scoring table:

225878 segs, 69334122 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb112 Database:

1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human 5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle 5:sp\_bhage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified 13:sp\_vertebrate 14:sp\_virus

Mean 44.372; Variance 79.166; scale 0.560 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|               |       | æ              |                          |    |        |                        |           |
|---------------|-------|----------------|--------------------------|----|--------|------------------------|-----------|
| Result<br>No. | Score | Query<br>Match | Query<br>Match Length DB | DB | 10     | Description            | Pred. No. |
| 7             | 1343  | 96.9           | 193                      | 11 | 966880 | BCL-W.                 | 3.25e-277 |
| 7             | 638   | 46.0           | 233                      | 1  | 035844 | BCL2-LIKE (BCL-XL).    | 2.64e-113 |
| ٣             | 260   | 40.4           | 229                      | 9  | 002718 | BCL-2 (FRAGMENT).      | 1.15e-95  |
| 4             | 533   | 38.5           | 235                      | 1  | 035843 | BCL2-LIKE (BCL-X-GAMMA | 1.32e-89  |
| S             | 207   | 14.9           | 170                      | 11 | Q9WUI5 | BCL-X SHORT.           | 5.41e-20  |
| 9             | 182   | 13.1           | 213                      | 11 | 035425 | BCL-2-RELATED OVARIAN  | 3.16e-15  |
| 7             | 177   | 12.8           | 331                      | 11 | P97287 | EAT/MCL-1 PROTEIN (MCL | 2.70e-14  |
| 80            | 176   | 12.7           | 170                      | 11 | 088857 | BCL-2-RELATED OVARIAN  | 4.14e-14  |
| σ             | 175   | 12.6           | 172                      | 11 | 055177 | B-CELL LEUKEMIA/LYMPHO | 6.35e-14  |
| 10            | 174   | 12.6           | 172                      | 11 | 055179 | B-CELL LEUKEMIA/LYMPHO | 9.71e-14  |
| 11            | 174   | 12.6           | 174                      | 13 | Q9W6F2 | PROTEIN A1.            | 9.71e-14  |
| 12            | 175   | 12.6           | 330                      | 1  | Q921P3 | MCL-1 PROTEIN.         | 6.35e-14  |
| 13            | 168   | 12.1           | 211                      | 13 | Q9W6F1 | MYELOID CELL LEUKEMIA  | 1.23e-12  |
| 14            | 144   | 10.4           | 80                       | 9  | 077738 | BAK PROTEIN (FRAGMENT) | 2.28e-08  |
| 15            | 120   | 8.7            | 128                      | 11 | 055178 | B-CELL LEUKEMIA/LYMPHO | 2.21e-04  |
| 16            | 117   | 8.4            | 923                      | 4  | Q9Y3R2 | NUCLEAR TRANSPORT RECE | 6.59e-04  |
| 17            | 103   | 7.4            |                          | 14 | 036423 | SIMILAR TO BCL-FAMILY  | 8.67e-02  |
| 18            | 103   | 7.4            | 521                      | 14 | Q9YTU1 | GAG PROTEIN,           | 8.67e-02  |
| 19            | 102   | 7.4            | 1259                     | Ŋ  | 044971 | C42C1.4 PROTEIN.       | 1.21e-01  |
| 70            | 100   | 7.2            | 630                      | 'n | 024222 | METALLOPEPTIDASE.      | 2.34e-01  |

181 GALVTVGAFFASK 193

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| 3.25e-01<br>4.50e-01<br>4.50e-01<br>6.22e-01<br>6.22e-01<br>6.22e-01<br>6.22e-01<br>6.22e-01<br>1.62e+00<br>1.62e+00<br>1.62e+00<br>1.62e+00<br>1.62e+00<br>1.62e+00<br>2.21e+00   | 2.21e+00<br>2.21e+00<br>4.10e+00<br>4.10e+00<br>3.01e+00<br>4.10e+00<br>4.10e+00   |
|--|--|
| ORF 16. BCL-2 HOMOLOG. TRANSPORTIN-SR. MORPHINE 6-DEHYDROGENA TERMINAL PROTEIN. 798AA LONG HYPOTHETICA D2013.5 PROTEIN. PKS MODULE 4. LATENT TGF BETA BINDIN SEROUTYPE B POTATIVE MA HYPOTHETICAL 32.3 KD P HYPOTHETICAL 32.3 KD P SEQUENCE OF BAC F21M12 PUTATIVE RNA DEPENDENT FATTY ACID SYNTHASE (E NODJ. AAOAA LONG HYPOTHETICA | GLYPICAN 6.  HYPOTHERICAL 70.8 KD P TRANSALDOLASE 1 (EC 2. 2. TRANSALDOLASE (EC 2. 2. CIS, CIS, CIS-MCONATE TRANS CONSERVED PROTEIN (FLP MOLYBDOPPERIN OXIDORED R31.1 PROTEIN. |
| P90504<br>Q9WRTG<br>Q9Y5L0<br>Q9Y657<br>Q9Y0657<br>Q990657<br>Q099154<br>Q098349<br>Q098349<br>Q097148<br>Q097312<br>Q04846<br>Q02312  | 007152<br>007192<br>0007192<br>000751<br>0027209<br>030061   |
| 444 24 1 2 2 1 1 2 2 2 2 2 2 2 2 2 2 2 2   | 42142112   |
| 175<br>175<br>175<br>175<br>1713<br>1713<br>1713<br>1713<br>1713   | 555<br>657<br>140<br>337<br>413<br>505<br>896<br>4101  |
| 7777777799999999977  |  |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0  | 911111111111111111111111111111111111111  |
| 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2  | 338<br>338<br>441<br>442<br>444<br>544   |
|  |  |

#### ALIGNMENTS

| RESULT | ונד ז                                 |   |               |                                   |  |   |
|--------|---------------------------------------|---|---------------|-----------------------------------|--|---|
| Q S    | 966880                                | PRELIMINARY;  | PRT;          | 193 AA.                           |  |   |
| Y Y    | 088996;                               |   |               |                                   |  |   |
| i b    | 01-NOV-1998                           | (TremBirel 08,  |               | Created)<br>Last sequence undate) |  |   |
| ដ      | 01-NOV-1999                           | (TrEMBLrel.   | Last          | annotation update)                |  |   |
| DE     | BCL-W.                                |   |               | •                                 | •  |   |
| GN     | BCL-W.                                |   |               |                                   |  |   |
| SO     | Rattus norve                          | Rattus norvegicus (Rat).                                |               |                                   |  |   |
| 8      | Eukaryota; M                          | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;     | a; Craniat    | ta; Vertebrata                    | ı; Mammalia;   |   |
| ဗ      | Eutheria; Rodentia;                   | dentia; Sciurog   | nathi; Mu     | Sciurognathi; Muridae; Murinae;   | e; Rattus.   |   |
| RN     | Ξ                                     |   |               |                                   |  |   |
| RP     | SEQUENCE FROM N.A.                    | M N.A.  |               |                                   |  |   |
| 2      | STRAIN-SPRAG                          | STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;                    | UE=BRAIN;     |                                   |  |   |
| RA     | HAMNER S., S                          | HAMNER S., SKOGLOSA Y., LINDHOLM D.;                    | DHOLM D.;     |                                   |  |   |
| RT     | "Differentia                          | "Differential expression of Bcl-w                       | Bcl-w and     | d Bcl-x mRNA i                    | Bcl-x mRNA in the developing and   |   |
| RT     | adult nervous                         | is system.";  |               |                                   | 1  |   |
| RL     | Submitted (0                          | Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases | EMBL/GenI     | Bank/DDBJ data                    | ibases.  |   |
| DR     | EMBL; AF0962                          | EMBL; AF096291; AAC64200.1;                             | •             |                                   |  |   |
| DR     | HSSP; P53563; 1AF3                    | 1; IAF3.  |               |                                   |  |   |
| DR     | PROSITE; PS0                          | PS01080; BH1; 1.  |               |                                   |  |   |
| DR     |                                       | PS01258; BH2; 1.  |               |                                   |  |   |
| DR     |                                       | PS01260; BH4_1; 1.                                      |               |                                   |  |   |
| DR     | PFAM; PF0045                          | PFAM; PF00452; Bcl-2; 1.                                |               |                                   |  |   |
| SQ     | SEQUENCE 1                            | 193 AA; 20820 MW;                                       |               | 6E5F84BA CRC32;                   | •  | , |
| ā      | Onerv Watch                           | • 80 yb   | Score 1343.   | . 11 ad                           | Length 193.  |   |
| žä     | Query maccii<br>Bost Local similarity |   | Dred No       | 250-277.                          | יכוז רוו דיייי   |   |
| ž      | Matches 184;                          | ?   | 7; Mismatches | natches 1;                        | Indels 1; Gaps 1   | н |
| ΟQ     | 1 MATPAST                             | PDTRALVADFVGYKL   | ROKGYVCGAC    | SPGEGPAADPLHO                     | MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60                            |   |
| δy     | :     <br>  MPTPAST                   |   | RQKGYVCGAC    |                                   | :  |   |
| Ę      | 61 FCDLAA                             | THVPDGGAOORFFOV   | CDET.FORCE    | MACRINA PEVEGA                    | ESDI. A A OLHVIT DE SA O ORFITO V SDET. FOR GEDNIAGRI VA FEVERA A L'A ESVNIKEMEDI. VG. 130 |   |
| 3      |                                       |   |               |                                   |  |   |
| ΟŸ     | 61 FSDLAAQ                            | LHVTPGSAQQRFTQV   | SDELFOGGP     | NWGRLVAFFVFGA                     | FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120                           |   |
| qq     | 121 OVQDWMV                           | TYLETRLADWIHSSG   | GWAEFTALYC    | SDGALEEARRLREC                    | QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180                           |   |
| ò      | 121 QVQDWIV                           | :   | :             |                                   |  |   |
| ı      |                                       |   |               |                                   |  |   |

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:: ||:| |||||| |:||:|||::|||:|||:|| | | | | |:||: | ||||:||| | | ||| |||:|||| 41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 SFGGALCVESYDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
                                                                                                                                                                                                                                                                                                                                                                                                                   85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
                                                                                                                                                                                                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                                                                                      Ouery Match 44.9%; Score 623; DB 1; Length 233; Best Local Similarity 52.4%; Pred. No. 7.82e-45; Matches 76; Conservative 34; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: KORSMETER, Stanley J.
TITLE OF INVENTION: BCI-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
STREET: 379 Lytton Avenue
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
AURIENT APPLICATION DATA:
AUBLICATION NUMBER: US/08/081,448
FILING DATE: 19930622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 AA
                                                                                   FILING DATE: 1993062
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646008thrup, Thomas E.
REGISTRÁTION NUMBER: 33,268
REGISTRÁTION NUMBER: 33,268
REEPROKE/DOCKET NUMBER: ARCD090
TELECOMMUNICATION INFORMATION:
TELEPRAN: 312-755-4489
INFORMÁTION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
-SEQUENCE '233 AA; 26063 WW; 275311 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/661,479 FILING DATE: 11-UW-1995 CLASSIFICATION: 43 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 59, Application US/08661479 Patent No. 5834209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 59, Application US/08661479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::| | |:::| ||:|
161 RLREG-N-WAVSTV-VTGAVALGAL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 KGQERFÜRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JT 15
US-08-661-479-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 VFGAALCAESVNKEMEPLVGQVQDMIVAYLETRLADMIHSSGGWADFTALYGDGALEDAR 160
                                                                                                                                                                                                                                                                                                                                                                                                                        3; Gaps
                                                                                                                                                                                                                                                                                                                                                                          Match 44.9%; Score 623; DB 2; Length 233; Local Similarity 52.4%; Pred. No. 7.82e-45; les 76; Conservative 34; Mismatches 32; Indels
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REERBRUNE/ADCKET NUMBER: 15726A-000700
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LEGGTH: 233 amino acids
                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
JENCE 233 AA; 26049 MW; 275801 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 KGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::| | | :: : | | |:|
161 RLREG-N-WAVSTV-VTGAVALGAL 182
                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Search completed: Fri Jun 23 14:20:05 2000 Job time: 9 secs.

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STANDARD;
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Best Local Similarity 52.4%;
Matches 76; Conservative
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                                            94301
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US-08-081-448-6
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                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BARR, PHILIP J.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                  э;
Э
                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                        145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
                                                                                                                                                                                                                                                                                                                                                                                  3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 59, Application US/08333565
Patent No. 5622852
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                              Score 623; DB 3; Length 233; Pred. No. 7.82e-45; 34; Mismatches 32; Indels
                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 AA.
                                                                                                                                                                                                                                            23647-20007.20
                                                                                                                                                           APPLICATION NUMBER: US/08/471,057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                              233 AA; 26049 MW; 275801 CN;
                                            ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                               08/320,157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 59, Application US/08333565
                                                                                                                                                                                                                         NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 2364
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 KGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                       TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/32
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                               44.9%;
Local Similarity 52.4%;
Les 76; Conservative
                            NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                Palo Alto
California
                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                  COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-333-565-59
                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                Query Match
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85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 623; DB 1; Length 233;
Pred. No. 7.82e-45;
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5646008th Clark Street, Suite 800
CITY: Chicago
                                                                                                                                                               COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION NOTA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
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Patent No. 5646008
GENERAL INFORMATION
APPLICANT: Thompson, Craig B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: peptide
JENCE 233 AA; 26049 MW; 275801 CN;
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                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION UNDRER: 30,223
REFERENCE/DOCKET UNDRER: 15726
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08081448
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TYPE: amino acid
STRANDEDNESS: single
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                          3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 623; DB 4; Length 233; Pred. No. 7.82e-45; 34; Mismatches 32; Indels
                                                                                          TITLE OF INVENTION: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDAGES:
ADDAGESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 AA.
 233 AA
                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/081.448
FILING DATE: 22 JUNE 1993
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET UNMBER: ARCD090
TELECOMMUNICATION INFORMATION:
TELECPHONE: 512-320-7200
                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US94/07089 FILING DATE: CONCURRENTLY FILED
                                                                                                                                                              United States of America
PRT;
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
TRNCE 233 AA; 26049 MW; 275801 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                  Sequence 7, Application PC/TUS9407089 GENERAL INFORMATION:
                                                  Sequence 7, Application PC/TUS9407089
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                                                                                                                                                                                                                                                                                                                        TELEFAX: 713-789-20/>
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 KGQERFNRWFLTGMTVAGVVLLGSL 229
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TELEPHONE: 713-789-2679
                                                                                                                                                                                COMPUTER READABLE FORM:
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Best Local Similarity 52.4%;
Matches 76; Conservative
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                                                                                                                                             CITY: Houston
                                                                                                                                                              COUNTRY: Un
PCT-US94-07089-7
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                                                                                   APPLICANT:
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85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Gaps
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                                                                                                                                                                                                                                                                                     STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DARE: US/08/470,670A
GENERAL INFORMATION:
APPLICANT: Thompson, Craig B. B.
APPLICANT: Thompson, Craig B. B.
TITLE OF INVENTION: LAWIENCE H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 AA
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JENCE 233 AA; 26063 MW; 275311 CN;
  Sequence 7, Application US/08470670A Patent No. 5834309
Patent No. 5834309 5710045
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Patent No. 6015697
GENERAL INFORMATION:
APPLICANT: KIEFER, MICHAEL C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Highlander, Steven L.
REGIZTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 474-757
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/08471057
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TOPOLOGY: li-
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PRIOR APPLICATION DATA:
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Matches 76; Conservative
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                                 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
         62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
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                                                                                                                                                                                                                                                                E: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                             TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2 TITLE OF INVENTION: Homologue
                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/798,897 FILING DATE: February 11, 1997
                                                                                                                         192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                          1483.0140001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
ENCE 192 AA; 20701 MW; 181510 CN;
                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                           Sequence 6, Application US/08798897
Patent No. 5789201
GERERAL INFORMATION:
APPLICANT: Guastella, John
                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INPORMATION:
NAME: ESEMON RODERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2540
                                                                                                                                                                            Sequence 6, Application US/08798897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEGUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                         STANDARD;
                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                  Washington
                                                                     181 ALVTVGAFFASK 192
                                                                              181 ALVTVGAFFASK 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 623; DB 4; Length 233;
Pred. No. 7.82e-45;
34; Mismatches 32; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24, Application PC/TUS9504600
GENERAL INFORMATION:
APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION
TITLE OF INVENTION: Interaction of Proteins Involved in
TITLE OF INVENTION: a Cell Death Pathway
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                  233 AA.
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                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
CE 233 AA; 26063 MW; 275311 CN;
                                                                                                                                                                                                                                                                                                                                                Sequence 24, Application PC/TUS9504600
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TELECOMMUNICATION INFORMATION:
TELEFONE: (619) 535-9001
TELEFONE: (619) 535-9049
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Imbra, Richard J.
REGISTRATION NUMBER: 37,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 KGQERFNRWFLTGMTVAGVVLLGSL 229
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Best Local Similarity 52.4%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Diego
STATE: California
                                                                                         181 ALVTVGAFFASK 192
                                                                                                                181 ALVTVGAFFASK 192
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STRANDEDNESS: not
TOPOLOGY: linear
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                                    SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
                                                                        121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
                                                                                   62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
1 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRTF 60
         2 PTPASTPDFRALVADFVGYRLRQKGYVCGAGPGEGPAADPLEQAMRAAGDEFETRFRRTF 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                      AUDICESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600 CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 192;
                                                                                                                                                                                                                                             Sequence 5, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICART Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1332; DB 1; I
Pred. No. 7.67e-110;
7; Mismatches 1;
                                                                                                                                                                     192 AA
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FILING DATE: February 11, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
FENCE 192 AA; 20689 MW; 183185 CN;
                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 1483
TELECHOUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acids
                                                                                                                                                                                                                             Sequence 5, Application US/08798897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not relevant
                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.1%;
95.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                               181 ALVTVGAFFASK 192
                                                                                                                         181 ALVTVGAFFASK 192
                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                       20002
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                                                                                                                                                                    US-08-798-897-5
                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                          62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
                                                                                                  121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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Pred. No. 2.75e-109;
                                                                                                                                                                                                                                                                                                                                                         192 AA
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PRIOR APPLICATION 424
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATORNEY AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Mismatches
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FENCE 192 AA; 20701 MW; 181510 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08978523
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                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202-371-2540
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Best Local Similarity 94.3%;
Matches 181; Conservative
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                                              61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                        121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                  61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
          MATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                                         Sequence 4, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1337; DB 2; Length 193;
Pred. No. 2.65e-110;
8; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
                                                                                                                                                                  193 AA
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MOLECULE TYPE: protein
FENCE 193 AA; 20832 MW; 183365 CN;
                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-260
                                                                                                                                                                                                                          Sequence 4, Application US/08978523
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LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
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TELEPHONE: ZUZ ...
ZOZ-371-2540
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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Best Local Similarity 94.3%;
Matches 182; Conservative
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                       1 MATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
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Pred. No. 7.67e-110;
7; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDES: 53
CORRESPONDES: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIETCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIETCATION: 424
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JENCE 192 AA; 20689 MW; 183185 CN;
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Best Local Similarity 95.3%;
Matches 183; Conservative
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                                  1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                           Gaps
 Length 193;
                                                                                                                                                                                                                                                                                                                               ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600
                 Indels
                                                                                                                                                                                                                                                         Sequence 3, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICAMT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF SEQUENCE: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
Score 1343; DB 1; I
Pred. No. 7.37e-111;
7; Mismatches 1;
                                                                                                                                                                                          193 AA.
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CLASSIPFCATION: 44
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIPICATION: 44
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.01400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-260
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 193 AA; 20820 MW; 185063 CN;
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                                                                                                                                                                                                                                           Sequence 3, Application US/08978523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                         STANDARD;
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Query Match 96.9%;
Best Local Similarity 95.3%;
Matches 184; Conservative
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STATE: DC
COUNTRY: USA
                                                                                                                                      181 GALVTVGAFFASK 193
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                                                                                  1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                            1; Gaps
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                                                                                                       Sequence 4, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
Score 1343; DB 2; Length 193;
Pred. No. 7.37e-111;
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Pred. No. 2.65e-110;
8; Mismatches 2; Indels
                                          1; Indels
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SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 1483.0140001
TELEPOMUNICATION INFORMATION:
TELEPOMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 AA.
                                          7; Mismatches
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HENCE 193 AA; 20832 MW; 183365 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08798897
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 193 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
Query Match 96.9%;
Best Local Similarity 95.3%;
Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 94.3%;
Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                181 GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                   180 GALVTVGAFFASK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XXXXXX
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| * * *                                   | (TM)                                   | ***                                   |
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| *******                                 | '<br>    <sub> </sub>                  | *******                               |
| ******                                  | '' '-'<br>  <sub>1</sub>               | ********                              |
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| *****                                   | )> <u>}</u>                            | ********                              |
| * * *                                   |  | * * *                                 |

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protein - protein database search, using Smith-Waterman algorithm Fri Jun 23 14:19:56 2000; MasPar time 5.42 Seconds 511.832 Million cell updates/sec MPsrch\_pp Run on:

Tabular output not generated.

>US-09-155-327B-9 (1-192) from USO9155327B.pep 1386 1 MPTPASTPDTRALVADFVGY......VTGAVALGALVTVGAFFASK 192 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

Searched:

145341 seqs, 14437480 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5A\_COMB 2:5B\_COMB 3:6\_COMB 4:PCT\_COMB 5:backfiles1 Database:

Mean 30.635; Variance 141.077; scale 0.217 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Pred. No.                  | 7.37e-111   | 7.37e-111   | 2.65e-110  | 2.65e-110   | 7.67e-110   | 7.67e-110   | 2.75e-109   | 2.75e-109   | 7.82e-45     | 7.82e-45    | 7.82e-45    | 7.82e-45     | 7.82e-45     | 7.82e-45   | 7.82e-45     | 7.82e-45     | 7.82e-45     | 3.06e-39     | 3.06e-39     | 8.61e-39     | 8.61e-39     | 3            | 8.61e-39     |
|----------------------------|-------------|-------------|------------|-------------|-------------|-------------|-------------|-------------|--------------|-------------|-------------|--------------|--------------|------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|
| D                          | Applicatio  | Applicatio  | Applicatio | Applicatio  | Applicatio  | Applicatio  | Applicatio  | Applicatio  | Applicati    | Applicatio  | Applicatio  | Applicati    | Applicati    | Applicatio | Applicati    | Applicati    | Applicati    | Applicati    | Applicati    |              |              |              | Applicati    |
| Description                | Sequence 3, | Sequence 3, | 4,         | Sequence 4, | Sequence 5, | Sequence 5, | Sequence 6, | Sequence 6, | Sequence 24, | Sequence 7, | Sequence 7, | Sequence 14, | Sequence 59, | 9          | Sequence 59, | Sequence 14, | Sequence 24, | Sequence 23, | Sequence 23, | Sequence 10, | Sequence 10, | Sequence 10, | Sequence 10, |
| ID                         | -864-80-SD  | OS-08-978-  | us-08-798- | us-08-918-  | 0S-08-978-  | ns-08-198-  | us-08-978-  | -864-80-SD  | PCT-US95-0   | PCT-US94-0  | US-08-470-  | US-08-471-   | US-08-333-   | US-08-081- | US-08-661-   | US-08-471-   | - 209-80-sn  | us-08-607-   | PCT-US95-0   | us-08-337-   | us-08-826-   | US-08-248-   | ns-08-82e-   |
| DB                         | Н           | ~           | ٦          | ~           | ~           | -           | ~           | Н           | 4            | 4           | 7           | m            | Н            | Н          | ~            | -1           | Н            | ٦            | 7            | ~            | ~            | 7            | 7            |
| %<br>Query<br>Match Length | 193         | 193         | 193        | 193         | 192         | 192         | 192         | 192         | 233          | 233         | 233         | 233          | 233          | 233        | 233          | 233          | 233          | 233          | 233          | 239          | 239          | 239          | 239          |
| &<br>Query<br>Match        | 96.9        | 6.96        | 96.5       | 96.5        | 96.1        | 96.1        | 95.7        | 95.7        | 44.9         | 44.9        | 44.9        | 44.9         | 44.9         | 44.9       | 44.9         | 44.9         | 44.9         | 40.5         | 40.5         | 40.1         | 40.1         | 40.1         | 40.1         |
| Score                      | 1343        | 1343        | 1337       | 1337        | 1332        | 1332        | 1326        | 1326        | 623          | 623         | 623         | 623          | 623          | 623        | 623          | 623          | 623          | 561          | 561          | 556          | 556          | 226          | 556          |
| Result<br>No.              | 7           | 7           | ٣          | 4           | 2           | 9           | 7           | 8           | σ            | 10          | 11          | 12           | 13           | 14         | 15           | 16           | 17           | 18           | 19           | 20           | 21           | 22           | 23           |